

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 04:39:54 ; Search time 171.5 seconds
(without alignments)
302.017 Million cell updates/sec

Title: US-09-975-842-2

Sequence: 1 gnnpncngnttmgntng 23

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N.ceneseq_101002:*

1:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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22:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	67.3	23	AAV30328	ACC synthase gene
2	15.4	67.3	23	AAV30328	PCR primer #1 used
3	15.4	67.3	748	ABQ65439	Arabidopsis thaliana
4	15.4	67.3	961	AAV00220	1-aminocyclopropan
5	15.4	67.3	968	AAV00219	1-aminocyclopropan
6	15.4	67.3	993	AAV33139	Broccoli ACC synth
7	15.4	67.3	1080	AAV72628	Ananas comosus ACC
8	15.4	67.3	1096	AAV72631	Mangifera indica ACC
9	15.4	67.3	1098	AAV72630	Carica papaya ACC

10	15.4	67.0	1104	AAV72629	Carica papaya ACC
11	15.4	67.0	1113	AAV72632	Mangifera indica A
12	15.4	67.0	1170	AAV62647	ACC synthase gene-2
13	15.4	67.0	1384	AAV33136	Broccoli ACC synth
14	15.4	67.0	1482	AAV25896	ACC synthetase gen
15	15.4	67.0	1703	AAQ25896	Clone PACCI encodi
16	15.4	67.0	1703	AAQ15131	Zucchini ACC synth
17	15.4	67.0	1703	AAV15701	Zucchini 1-aminocy
18	15.4	67.0	1703	AAV04541	Zucchini ACC synth
19	15.4	67.0	1775	AAV23618	Clone PIACC1 encod
20	15.4	67.0	1780	AAQ15138	Clone PIACC5 encod
21	15.4	67.0	1781	AAQ15137	Clone PIACC4 encod
22	15.4	67.0	1793	AAQ15136	Clone PIACC3 encod
23	15.4	67.0	1793	AAQ15139	Clone PIACC6 encod
24	15.4	67.0	1800	AAV09713	ACC synthase DNA.
25	15.4	67.0	1818	AAQ15135	Clone PIACC2 encod
26	15.4	67.0	1818	AAQ04546	Tomato 1-aminocycl
27	15.4	67.0	1828	ABLO9571	Drosophila melanog
28	15.4	67.0	1868	AAV73502	Poplar 1-aminocycl
29	15.4	67.0	1878	AAV30326	Pelargonium 1-amin
30	15.4	67.0	1888	AAV31482	Papaya ACC synthas
31	15.4	67.0	1923	AAV29467	Mung bean ACC synt
32	15.4	67.0	2088	AAV20947	Collie fruit speci
33	15.4	67.0	2230	AAV15704	Tomato ACC synthas
34	15.4	67.0	2230	AAQ04544	Tomato ACC synthas
35	15.4	67.0	2230	AAV23621	Tomato ACC synthas
36	15.4	67.0	2438	AAV35671	DNA encoding a 1-a
37	15.4	67.0	5613	AAV05241	Crucifer 1-aminocy
38	15.4	67.0	6910	AAV05241	Drosophila melanog
39	15.4	67.0	7241	AAQ15140	Genomic clone LE-A
40	15.4	67.0	7244	AAV15705	Tomato ACC synthas
41	15.4	67.0	7244	AAQ04545	Tomato 1-aminocycl
42	15.4	67.0	7244	AAV23622	Tomato ACC synthas
43	15.4	67.0	7587	AAQ15133	Zucchini ACC synth
44	15.4	67.0	7587	AAV15703	Zucchini ACC synth
45	15.4	67.0	7587	AAQ04543	Zucchini CP-ACC 1B

ALIGNMENTS

RESULT 1
ID AAV30328 standard; DNA; 23 BP.
AC AAV30328;
XX
XX 28-SEP-1998 (first entry)
XX
DE ACC synthase gene PCR primer 1.
XX
XX ACC synthase: 1-aminocyclopropane-1-carboxylate synthase;
KW ethylene; transgenic plant; wilting; geranium; rose; PCR; primer;
KW ss.
XX
XX Synthetic.
OS Pelargonium x hortorum.
OS Rosa sp.
XX
XX
FH Key
FH modified_base 3 Location/Qualifiers
FT /*tag= a
FT /mod_base= i
FT modified_base 6
FT /*tag= b
FT /mod_base= i
FT modified_base 9
FT /*tag= c
FT /mod_base= i
FT modified_base 12
FT /*tag= d
FT /mod_base= i
FT modified_base 18

```

FT      /*lag= e
FT      /mod_base= i
FT      21
FT      modified_base
FT      /mod_base= i
XX
XX      W09814465-A1.
XX
XX      09-APR-1998.
XX
XX      30-SEP-1997; 97WO-US17644.
XX
XX      01-OCT-1996; 96US-0724194.
XX
XX      (COLS ) UNIV COLORADO STATE RES FOUND.
XX
XX      Ranu RS;
XX
XX      WPI: 1998-260994/23.
XX
XX      New isolated ACC synthase genes - are obtained from geranium and
XX      rose, used to develop products for producing plants with reduced
XX      ethylene levels, for increasing shelf-life
XX
XX      Example; Page 36; 77pp; English.
XX
XX      Primer I and primer II (see AAV30329) were used in PCR amplifications
XX      to develop PCR probes for the isolation of geranium and rose
XX      1-aminocyclopropane-1-carboxylate synthase (ACC synthase) cDNA
XX      clones (see AAV30324-26 and AAV30330). The invention relates to the
XX      use of antisense fragments of these genes to control ACC synthase
XX      expression in plants. By reducing the amount of ACC synthase
XX      produced in plant cells, the rate of ACC conversion to ethylene
XX      can be decreased. This can be used to prolong the shelf-life of
XX      cut flowers and to reduce leaf yellowing and petal abscission
XX      during shipping and storage.
XX
XX      Sequence 23 BP; 0 A; 2 C; 7 G; 4 T; 10 other;
XX
XX      Query Match 67.0%; Score 15.4; DB 19; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX      ||||||||||||||||||||
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX
XX      RESULT 2
XX      AAS19698
XX      ID AAS19698 standard: DNA; 23 BP.
XX
XX      AAS19698;
XX
XX      09-APR-2002 (first entry)
XX
XX      PCR primer #1 used to amplify DNA fragment of geranium pHSacc genes.
XX
XX      Geranium; 1-aminocyclopropane-1-carboxylate synthase gene promoter;
XX      ACC synthase; plant transcription regulation; plant; PCR: primer;
XX      gPHSacc49; ss.
XX
XX      Pelargonium x hortorum.
XX
XX      W0200185754-A1.
XX
XX      15-NOV-2001.
XX
XX      09-MAY-2001; 2001WO-US15023.
XX
XX      09-MAY-2000; 2000US-203021P.
XX      12-OCT-2000; 2000US-239782P.
XX

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```

PA      (COLS ) UNIV COLORADO STATE.
PA      (TAGA-) TAGAMA GREENHOUSES INC.
XX
XX      Ranu RS;
XX
XX      WPI: 2002-075241/10.
XX
XX      New promoter from the 1-aminocyclopropane-1-carboxylate synthase gene
XX      of geranium, useful to regulate level of transcription of coding
XX      sequence in geranium and other plants
XX
XX      Claim 7; Fig 2; 38pp; English.
XX
XX      The present invention relates to the isolation of promoter DNA from
XX      geranium (Pelargonium x hortorum) genomic clone pHSacc49 (gPHSacc49).
XX      This promoter represents the ACC (1-aminocyclopropane-1-carboxylate)
XX      synthase gene promoter. The promoter is useful to regulate the
XX      transcription level of a coding sequence in geranium and other plants.
XX      The present sequence represents a PCR primer used to amplify a DNA
XX      fragment of geranium pHSacc genes.
XX
XX      Sequence 23 BP; 0 A; 2 C; 7 G; 4 T; 10 other;
XX
XX      Query Match 67.0%; Score 15.4; DB 24; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX      ||||||||||||||||||||
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX
XX      RESULT 3
XX      AB065439/C
XX      ID AB065439 standard: DNA; 748 BP.
XX
XX      AB065439;
XX
XX      21-AUG-2002 (first entry)
XX
XX      Arabidopsis thaliana polynucleotide SEQ ID NO 16.
XX
XX      Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
XX      stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
XX      insecticide; antibiotic; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      US2002059663-A1.
XX
XX      16-MAY-2002.
XX
XX      26-JAN-2001; 2001US-0770149.
XX
XX      27-JAN-2000; 2000US-178506P.
XX
XX      (GORL/) GORLACH J.
XX      (ANY/) AN Y.
XX      (HAM/) HAMILTON C M.
XX      (PRIC/) PRICE J L.
XX      (RAIN/) RAINES T M.
XX      (YUY/) YU Y.
XX      (RAME/) RAMEAKA J G.
XX      (PAGE/) PAGE A.
XX      (MATH/) MATHEW A V.
XX      (LEDF/) LEDFORD B L.
XX      (WORS/) WORESSNER J P.
XX      (HAAS/) HAAS W D.
XX      (GARC/) GARCIA C A.
XX      (KRIC/) KRICKER M.
XX      (SLAT/) SLATER T.
XX      (DAVI/) DAVIS K R.
XX      (ALLE/) ALLEN K.

```

PA (HOFF/) HOFFMAN N.
 XX (HURB/) HURBAN P.
 PI Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 PI Rameek JG, Price A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CA, Kricker M, Slater T, Davis RK, Allen K, Hoffman N,
 PI Hurban P;
 DR WPI: 2002-47924/51.
 XX
 PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
 PT useful e.g. for preparing transgenic plants with increased resistance
 PT or altered metabolism
 XX
 PS Claim 1: SEQ ID NO 16: 40bp + Sequence Listing: English.
 CC The invention relates to nucleic acids (I) that hybridise under stringent
 CC conditions to any of 999 sequences (AB065424-AB066422) or their
 CC fragments. (II) are used to suppress the corresponding polypeptides (II) or
 CC to produce genetically modified plant cells or transgenic plants, which
 CC may have improved resistance to disease, stress, or altered
 CC metabolic/biosynthetic pathways (for production of commercial
 CC nutritional or medicinal products) or generally any trait of interest,
 CC insecticides and antibiotics) or biologically active agents (e.g. fungicides,
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docid=99909770149.
 XX
 SQ Sequence 748 BF: 209 A; 202 C; 120 G; 213 T; 4 other;
 Query Match 67.0%; Score 15.4; DB 24; Length 748;
 Best Local Similarity 56.5%; Pred. No. 1.5e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 GGNVTNCCNGNTTYMGNRTNG 23
 DB 617 GGCTCTCCGTTCGCGCGGG 595
 RESULT 4
 ID AAV00220 standard; DNA; 961 BP.
 XX
 AC AAV00220;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE 1-aminocyclopropane-1-carboxylic acid synthase gene acacc3.
 XX
 KW 1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
 KW flowering; inhibition; regulation; development; fruit; ss.
 XX
 OS Ananas comosus.
 XX
 XX Key Location/Qualifiers
 XX CDS 1..961
 XX FT /tag= a
 XX FT /product= "acacc3"
 XX FT /note= "no stop codon given; contains an intron"
 XX FT 1..101
 XX FT /tag= b
 XX FT /number= 1
 XX FT 102..193
 XX FT /tag= c
 XX FT /number= 1
 XX FT 194..961
 XX FT /tag= d
 XX FT /number= 2
 XX
 XX AU9719963-A.
 XX 06-NOV-1997.

XX
 PF 01-MAY-1997; 97AU-0019963.
 XX
 PR 01-MAY-1996; 96AU-0009582.
 XX
 PA (GOLD-) GOLDEN CIRCLE LTD.
 PA (QUE-) STATE QUEENSLAND.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Botella J, Sanewski G;
 XX
 DR WPI: 1998-009279/02.
 DR P-PSDB: AAW37445.
 XX
 PT New isolated ACC synthase genes from pineapples - used to generate
 PT transgenic pineapples in which the natural initiation of flowering
 PT is inhibited
 XX
 PS Claim 2: Fig 2: 37pp; English.
 CC The present sequence represents the nucleotide sequence encoding a
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of
 CC pineapple. The present invention describes a transgenic variety of
 CC pineapple in which initiation of flowering is inhibited, the variety
 CC comprising a nucleotide sequence encoding an ACC synthase enzyme where
 CC the nucleotide sequence is operably linked. In the sense or antisense
 CC orientation, to one or more regulatory pineapple sequences. The ACC
 CC synthase gene can be used to regulate pineapple plant development.
 CC Particularly for inhibiting initiation of flowering. Such plants can
 CC then be induced to flower in a narrow spectrum of time which would
 CC thereby decrease the spread of fruit maturity within a crop.
 XX
 SQ Sequence 961 BP: 235 A; 246 C; 247 G; 233 T; 0 other;
 Query Match 67.0%; Score 15.4; DB 19; Length 961;
 Best Local Similarity 56.5%; Pred. No. 1.5e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 GGNVTNCCNGNTTYMGNRTNG 23
 DB 567 GGCTCTCCAGGCTTCGCGCGG 589
 RESULT 5
 ID AAV00219 standard; DNA; 968 BP.
 XX
 AC AAV00219;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE 1-aminocyclopropane-1-carboxylic acid synthase gene acacc2.
 XX
 KW 1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
 KW flowering; inhibition; regulation; development; fruit; ss.
 XX
 OS Ananas comosus.
 XX
 XX Key Location/Qualifiers
 XX CDS 1..968
 XX FT /tag= a
 XX FT /product= "acacc2"
 XX FT /transl_except= (pos:967..968,aa:Val)
 XX FT /note= "no stop codon given"
 XX
 XX AU9719963-A.
 XX 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97AU-0019963.
 XX
 PR 01-MAY-1996; 96AU-0009582.
 XX

PA	(GOLD-) GOLDEN CIRCLE LTD.
PA	(UEE-) STATE QUEENSLAND.
PA	(UYOU) UNIV QUEENSLAND.
PI	Botella J, Sanewski G;
XX	
DR	WPI; 1998-009279/02.
DR	P-PsDB; AAM37444.
XX	
PT	New isolated ACC synthase genes from pineapples - used to generate transgenic pineapples in which the natural initiation of flowering is inhibited
XX	
PS	Claim 1; Fig 1; 37pp; English.
CC	
CC	The present sequence represents the nucleotide sequence encoding a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of pineapple. The present invention describes a transgenic variety of pineapple in which initiation of flowering is inhibited, the variety comprising a nucleotide sequence encoding an ACC synthase enzyme where the nucleotide sequence is operably linked, in the sense or antisense orientation, to one or more regulatory nucleotide sequences. The ACC synthase gene can be used to regulate pineapple plant development, particularly for inhibiting initiation of flowering. Such plants can then be induced to flower in a narrow spectrum of time which would thereby decrease the spread of fruit maturity within a crop.
SQ	Sequence 968 BP; 241 A; 235 C; 294 G; 198 T; 0 other:
	Query Match 67.0%; Score 15.4; DB 19; Length 968;
	Best Local Similarity 56.5%; Pred. No. 1.5e+02;
Matches	13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY	- 1 GCAGTTCNGGNTTYMGRITNGG 23 : : :
DG	571 GGCTCCTCCCGGTGGTTAGGGTTGG 593
RESULT 6	
AAT33139	
ID	AAT33139 standard; cDNA: 993 BP.
XX	AAT33139;
AC	
DT	07-DEC-1996 (first entry)
DE	Broccoli ACC synthase cDNA clone TA13.
XX	
KW	ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase; ethylene; shelf-life; Cucumis melo; melon; transgenic plant; antisense; broccoli; ss.
KW	
OS	Brassica oleracea.
XX	
Key	Location/Qualifiers
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FT	primer_bind /*tag= b /note= "primer RM4494"
FT	primer_bind 975..993
FT	/tag= C /note= "primer RM491"
XX	
PN	WO9621027-A1.
XX	
PD	11-JUL-1996.
XX	
PF	07-JUN-1995; 95WO-US07271.
XX	
PR	30-DEC-1994; 94US-0366992.
XX	
PA	(ASGR-) ASGROW SEED CO.

PI	XO
PT	XX
PI	Hoesnore ML, Carney KJ, Deng RZ, Reynolds JF, Ruttenclutter GE;
XX	
DR	WPI: 1996-334002/33.
DR	P-PsDB; AAR98599.
PT	DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of
PT	Brassica oleracea - used to regulate ethylene-dependent processes
PT	in plants, esp. to improve shelf life
XX	
PS	Claim 3; Fig6A-C; 50pp; English.
XX	
CC	Brassica oleracea cDNA clone TA13 (AA73137) codes for
CC	1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase)
CC	(AAR95599), an enzyme involved in ethylene biosynthesis. It was
CC	obtd. by PCR amplification (see also AA73140) of broccoli Floret
CC	cDNA. The PCR product was cloned into pCRII to obtain clone
CC	TA13. cDNA or genomic DNA (see also AA73136) can be inserted, in
CC	sense or antisense orientation, into an expression cassette and then
CC	transferred to a binary vector suitable for Agrobacterium-mediated
CC	plant transformation. The constructs permit control of the level of
CC	ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
CC	melo) and hence a control of maturation, ageing and shelf-life.
XX	
SQ	Sequence 993 BP: 269 A; 233 C; 253 G; 238 T; 0 other:
Query Match	67.0%; Score 15.4; DB 17; Length 993;
Best Local Similarity	56.5%; Pred. No. 1.5e+02;
Matches 13: Conservative 4; Mismatches 6; Indels 0; Gaps 0.	
OY	1 GGNYTNCNGGNTTYMGNRTNGG 23 : : :: : 621 GGTCTTCGCCGGTTTGCAATTGC 643
RESULT 7	
AAT72628	
ID	AAT72628 standard; DNA; 1080 BP.
AC	
XX	AAT72628;
DT	
XX	27-JAN-1998 (first entry)
DE	Ananas comosus ACC synthase, acaccl gene.
XX	
KW	ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; aacocl; ethylene biosynthesis; transgenic plant; senescence; KW antisense expression system; plant development; fruit ripening; EC 4.4.1.14; pineapple; ss. XX
OS	Ananas comosus.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1080
FT	/tag= a
FT	/product= acaccl
FT	/EC_number= 4.4.1.14
FT	/note= "Sequence represents 75% of the coding sequence and does not contain the start or stop codons."
PN	WO9711166-A1.
XX	
PD	27-MAR-1997.
XX	
PF	20-SEP-1996; 96WO-AU00591.
XX	
PR	02-MAY-1996; 96AU-0009603.
XX	
PA	20-SEP-1995; 95AU-0005559.
XX	
PI	(UYOU) UNIV QUEENSLAND. Botella JR;

```
XX WPI: 1997-202875/18.
DR P-PSDB; AAW18236.
XX
PT Pineapple, papaya and mango ACC synthase genes - used in gene
XX therapy to produce fruits with reduced senescence
XX
PS Claim 1; Fig 1; 46pp; English.
XX
CC This sequence represents a novel gene, accac1, which encodes an ACC
CC synthase. The enzyme ACC synthase is involved in the pathway for ethylene
CC biosynthesis and the rate of endogenous expression of ACC synthase
CC is considered to limit substantially the rate of ethylene production.
CC Endogenous ethylene is often deleterious to crops, especially if some
CC form of mechanical wounding has occurred and diminishes their post
CC harvest quality and storage life. Novel ACC synthase genes expressed
CC in transgenic plants using either sense or antisense expression system
CC may be used to control the regulation of plant development, in
CC particular fruit ripening, reducing senescence and thus improving
CC storage life.
XX
SQ Sequence 1080 BP; 264 A; 294 C; 299 G; 223 T; 0 other;
Query Match 67.0%; Score 15.4; DB 18; Length 1080;
Best Local Similarity 56.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 GGNATNCNCNGITTYMGRTNGG 23
DB 691 GGTCTCCCGCGATTCCGAGTCGG 713
RESULT 8
AAT72631
ID AAT72631 standard; DNA; 1096 BP.
XX
AC AAT72631;
XX
DT 27-JAN-1998 (first entry)
XX
DE Mangifera indica ACC synthase miaccl gene.
XX
KM ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KM miaccl; ethylene biosynthesis; transgenic plant; senescence;
KM antisense expression system; plant development; fruit ripening;
KM EC 4.4.1.14; mango; multigene family; ss.
XX
OS Mangifera indica;
XX
FH Key Location/Qualifiers
FH CDS 1..1096
FT /*tag= a
FT /product= miaccl
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FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."
XX
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XX
PD 27-MAR-1997.
XX
PF 20-SEP-1996; 36WO-AU00591.
XX
PR 02-MAY-1996; 36AU-0009603.
PR 20-SEP-1995; 35AU-0005559.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Botella JR;
XX
DR WPI: 1997-202875/18.
DR P-PSDB; AAW18289.
PT
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```
XX Pineapple, papaya and mango ACC synthase genes - used in gene
PT therapy to produce fruits with reduced senescence
XX
PS Claim 4; Fig 4; 46pp; English.
XX
CC This sequence represents a novel gene, miaccl, which is a member
CC of an ACC synthase multigene family found in mango. ACC synthase is
CC involved in the pathway for ethylene biosynthesis and the rate of
CC endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.
XX
SQ Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;
Query Match 67.0%; Score 15.4; DB 18; Length 1096;
Best Local Similarity 56.5%; Pred. No. 1.6e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 GGNATNCNGGNTTYMGRTNGG 23
DB 688 GGCTCCCTCGCCTTAGCGTTGG 710
RESULT 9
AAT72630
ID AAT72630 standard; DNA; 1098 BP.
XX
AC AAT72630;
XX
DT 27-JAN-1998 (first entry)
XX
DE Carica papaya ACC synthase capacc2 gene.
XX
KM ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KM capacc2; ethylene biosynthesis; transgenic plant; senescence;
KM antisense expression system; plant development; fruit ripening;
KM EC 4.4.1.14; papaya; multigene family; ss.
XX
OS Carica papaya.
XX
FH Key Location/Qualifiers
FH CDS 1..1098
FT /*tag= a
FT /product= capacc2
FT /EC_number= 4.4.1.14
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."
XX
PN WO9711166-A1.
XX
PD 27-MAR-1997.
XX
PF 20-SEP-1996; 96WO-AU00591.
XX
PR 02-MAY-1996; 96AU-0009603.
PR 20-SEP-1995; 95AU-0005559.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Botella JR;
XX
DR WPI: 1997-202875/18.
DR P-PSDB; AAW18288.
PT Pineapple, papaya and mango ACC synthase genes - used in gene
therapy to produce fruits with reduced senescence
```

PS Claim 3; Fig 3; 46pp; English.

XX

CC This sequence represents a novel gene, *capac2*, which is a member
CC of the ACC synthase multigene family found in papaya. The enzyme ACC
CC synthase is involved in the pathway for ethylene biosynthesis and the
CC rate of endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.

XX

SQ Sequence 1098 BP; 276 A; 275 C; 299 G; 248 T; 0 other;

OY 1 GGATNCCNGGNTTGMNRTNGG 23
||:|||||:|:|:|:|:|:|:|:|
Db 688 GGCTCTCCCGGTTCCGGGTAGG 710

RESULT 10
AAT72629
ID AAT72629 standard; DNA; 1104 BP.

XX
AC AAT72629;

XX
DT 27-JAN-1998 (first entry)

XX
DE Carica papaya ACC synthase *capac1* gene.

XX
KM ACC synthase: S-adenosyl-L-methionine methylthioadenosine lyase;
KM *capac1*; ethylene biosynthesis; transgenic plant; senescence;
KM antisense expression system; plant development; fruit ripening;
KM EC 4.4.1.14; papaya; multigene family; ss.

XX
OS Carica papaya.

XX
FH Key Location/Qualifiers
FT 1..1104
FT CDS /tag= a
FT /EC_number= 4.4.1.14
FT /product= *capac1*
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."

XX
XX
PN WO9711166-A1.

XX
PD 27-MAR-1997.

XX
PF 20-SEP-1996; 96WC-AU00591.

XX
PR 02-MAY-1996; 96AU-0009603.
PR 20-SEP-1995; 95AU-0005559.

XX
PA (UYQU) UNIV QUEENSLAND.

XX
PI Botella JR;

XX
DR WPI; 1997-202875/18.
DR P-PDB; AAM18287.

XX
PT Pineapple, papaya and mango ACC synthase genes - used in gene
PT therapy to produce fruits with reduced senescence

PS Claim 2; Fig 2; 46pp; English.

XX

[illegible]

CC endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.

XX Sequence 1113 BP: 320 A; 212 C; 264 G; 317 T; 0 other:

QY Query Match 67.0%; Score 15.4; DB 18; Length 1113;
Best Local Similarity 56.5%; Pred. No. 1.6e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0.

1 GCATYCCNCIGATYMGATNGS 23
||:|||||:||||:|
Db 694 GCGTCCACGCTTAGGTCGG 716

RESULT 12
AAT66247 strand: DNA; 1170 BP.
XX AAT66247:
XX AAT66247:
XX 28-JUL-1997 (1st entry)
DE ACC synthase GAC-2 DNA.
XX ACC synthase: 1-aminocyclopropane-1-carboxylate synthase; antisense;
KM ethylene; transgenic plant; Petalagonium x domesticum.
XX In vitro propagation; tissue culture; ripening; ss.
XX Not identified.
XX OS
XX Not identified.
XX W09717429-AL.
XX 15-MAY-1997.
XX 08-NOV-1996; 96MO-US17954.
XX 09-NOV-1995; 95US-0555755.
XX (OGLEE-) OGEEVEE LTD.
XX (PENN-) PENN STATE RES FOUND.
XX Arteea J, Arteea RN, Ogleevee O'Donovan W, Stoots E;
XX WPI: 1997-281013/25.
XX P-PSDB: AAM09873.
XX Commercial propagation of transgenic plants by tissue culture -
XX especially Petalagonium x domesticum with decreased ethylene
XX formation
XX Claim 14, Page 34; 36pp: English.

XX 2 DNA sequences (AAT66246-47) respectively code for
CC 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1
CC (AAM09876) and GAC-2 (AAM09879), enzymes involved in the biosynthesis
CC of ethylene in plants. In a method for the commercial production
CC of transgenic plants, Agrobacterium vectors carrying antisense
CC genes for ACC synthase or ACC oxidase (see also AAT66248) are used
CC to inoculate petiole explants of a mother plant, pref.
CC Petalagonium x domesticum. The resulting callus is cultured and
CC used to regenerate transgenic plants. The antisense genes prevent
CC ACC synthase or ACC oxidase expression and hence ethylene
CC formation and fruit ripening.

XX Sequence 1170 BP: 319 A; 263 C; 297 G; 291 T; 0 other:

Query Match 67.0%; Score 15.4; DB 18; Length 1170;

Oy		Best Local Similarity: 56.5%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;		
DB	1 GGATNTCCNGCNTTGMNRTNGC 23 : 763 GCCTTCCTCGGCTTCAGGATGG 785	
RESULT 13		
ID	AAT33136	AAT33136 standard; DNA; 1384 BP.
AC	AAT33136;	
DT	07-DEC-1996	(first entry)
DE	Broccoli ACC synthase genomic DNA clone ACCA1.	
KW	ACC synthase; L-aminoacylpropyl-L-carboxylic acid synthase; ethylene; shelf-life; Cucumis melo; melon; transgenic plant; antisense; broccoli; ss.	
KX		
OS	Brassica oleracea.	
XX		
Key	Location/Qualifiers	
EH	Primer_bind	complement (1..31)
FT	/tag= a	
FT	/note= "primer RMK393"	
FT	exon	1..37
FT	/tag= b	
FT	/codon_start= 2..4	
FT	intron	38..134
FT	exon	/tag= c 135..431
FT	intron	/tag= d 432..594
FT	exon	/tag= e 595..1384
FT	exon	/tag= f 1352..1382
FT	primer_bind	/note= "primer RMK394"
FT		
PM	W09621027-A1.	
XX	11-JUL-1996.	
PD		
XX	07-JUN-1995; 95WO-US07271.	
PF		
XX	30-DEC-1994; 94US-0366992.	
PR		
XX	(ASGR-) ASGROW SEED CO.	
PA		
XX	Boeshore ML, Carney KJ, Deng RZ, Reynolds JF, Rutencutter GE;	
PI	WPI; 1996-334002/3.	
DR	P-PSDB; AAR98598.	
XX	DNA encoding L-amino:cyclo:proplyl-L-carboxylic acid synthase of	
PT	Brassica oleracea - used to regulate ethylene-dependent processes	
PT	in plants, esp. to improve shelf life	
XX		
PS	Claim 2; Fig1A-B; 50BP; English.	
XX		
CC	Brassica oleracea genomic clone ACCA1 (AAT33136) codes for	
CC	L-aminoacylpropyl-L-carboxylic acid synthase (ACC-synthase)	
CC	(AAR98598), an enzyme involved in ethylene biosynthesis. It was	
CC	obtd. by subjecting broccoli leaf total genomic DNA to PCR using	
CC	primers (see also AAT33137-38) based on the Arabidopsis thaliana ACC	
CC	synthase gene. The product was cloned into pCRIT to obtain clone	
CC	ACCA1. Genomic DNA or cDNA (see also AAT33139) can be inserted, in	
CC	sense or antisense orientation, into an expression cassette and then	
CC	transferred to a binary vector suitable for Agrobacterium-mediated	

CC plant transformation. The constructs permit control of the level of
 CC ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
 CC melo) and hence a control of maturation, ageing and shelf-life.
 XX
 SQ Sequence 1384 BP; 401 A; 290 C; 310 G; 383 T; 0 other;

Query Match 67.0%; Score 15.4; DB 17; Length 1384;
 Best Local Similarity 56.5%; Pred. No. 1.6e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNVTNCNGNNTYMGNRTNG 23
 DB 970 GGCTTCCTCCGTTTCGAGTTGG 992

RESULT 14
 ID AAQ25896 standard; cDNA; 1482 BP.
 XX
 AC AAQ25896;

XX 18-JAN-1993 (first entry)
 XX
 DE ACC synthetase gene.

XX 1-aminocyclopropane-1-carboxylic acid synthetase; detriment;
 KM ethylene; growth; maturity; aging; plant; ss.

XX Cucurbita maxima.

XX JF04169183-A.

XX 17-JUN-1992.

XX 31-OCT-1990; 90JP-0296943.

XX 31-OCT-1990; 90JP-0296943.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX WPI: 1992-253389/31.

XX P-PSDB; AAR25406.

XX Detriment induced ACC synthetase gene - used for control of
 PT bio-synthesis of ethylene, for controlling growth, maturity and
 XX ageing of higher plant

XX Claim 3; Fig 1; 10pp; Japanese.

XX The gene encoding detriment induced 1-aminocyclopropane-1-carboxylic
 CC acid (ACC) synthetase (EC 4.4.1.14) was obtd. by screening a cDNA
 CC library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from
 CC cDNA library clones was screened by an antibody method to identify
 CC colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.
 CC Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene
 CC controls the growth, maturing and aging of higher plants.

XX Sequence 1482 BP; 415 A; 341 C; 344 G; 382 T; 0 other;

Query Match 67.0%; Score 15.4; DB 13; Length 1482;
 Best Local Similarity 56.5%; Pred. No. 1.6e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNVTNCNGNNTYMGNRTNG 23
 DB 844 GGCTTCCTCCGTTTCGAGTTGG 866

RESULT 15
 ID AAQ15131 standard; cDNA; 1703 BP.
 XX
 AC AAQ15131;

XX 17-DEC-2001 (updated)
 DT 09-MAR-1992 (first entry)

XX Clone pACC1 encoding the Zucchini ACC synthase.

XX 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening;
 KW courgette; ss.

XX Cucurbita pepo.

XX key Location/Qualifiers
 FT CDS 11..1492
 FT /*tag= a
 FT /EC_number= 4.4.1.14
 FT 1683..1688
 FT /*tag= b

XX misc_signal

XX USN7579896-N.

XX 12-NOV-1991.

XX 10-SEP-1990; 90US-0579896.

XX 10-SEP-1990; 90US-0579896.

XX (USDA) US SEC OF AGRICULTURE.

XX Theologis A, Sato T;

XX WPI: 1991-368895/50.

XX P-PSDB; AAR15504.

XX DNA encoding ACC synthase - used for control of plant development
 PT and for prodn. of ACC synthase, ethylene and ethanol

XX Disclosure; Fig 1B; 73pp; English.

XX The ACC synthase cDNA was isolated from C. pepo using a novel method.
 CC A cDNA expression library was prepared from induced plant tissue.
 CC The library was screened with an antibody preparation obtained by
 CC partially purifying the induced ACC synthase and using it to
 CC immunise a suitable mammal. Immunoreactive clones were isolated and
 CC sequenced. One of these, pACC1, contained an open reading frame
 CC corresponding to a protein of 493 amino acids and mol. wt.
 CC 55,779 kD. See also AAQ15132-015140.

CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpl/updates/ntis-us.html.)

XX Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;

Query Match 67.0%; Score 15.4; DB 12; Length 1703;
 Best Local Similarity 56.5%; Pred. No. 1.6e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNVTNCNGNNTYMGNRTNG 23
 DB 854 GGCTTCCTCCGTTTCGAGTTGG 876

Search completed: March 10, 2003, 05:25:14
 Job time: 179.5 secs


```

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FT      /mod_base= i
XX
XX      WO9814465-A1.
XX
XX      09-APR-1998.
XX
XX      30-SEP-1997; 97WO-US17644.
XX
XX      01-OCT-1996; 96US-0724194.
XX
XX      (COLS ) UNIV COLORADO STATE RES FOUND.
XX
XX      Ranu RS:
XX      WPI; 1998-260994/23.
XX
XX      New isolated ACC synthase genes - are obtained from geranium and
XX      rose, used to develop products for producing plants with reduced
XX      ethylene levels, for increasing shelf-life
XX
XX      Example: Page 37; 77pp; English.
XX
XX      Primer II and primer I (see AAV30328) were used in PCR amplifications
XX      to develop PCR probes for the isolation of geranium and rose
XX      1-aminocyclopropane-1-carboxylate synthase (ACC synthase) cDNA
XX      clones (See AAV30324-26 and AAV30330). The invention relates to the
XX      use of antisense fragments of these genes to control ACC synthase
XX      expression in plants. By reducing the amount of ACC synthase
XX      produced in plant cells, the rate of ACC conversion to ethylene
XX      can be decreased. This can be used to prolong the shelf-life of
XX      cut flowers and to reduce leaf yellowing and petal abscission
XX      during shipping and storage.
XX
XX      Sequence 23 BP; 5 A; 5 C; 0 G; 1 T; 12 other:
XX
XX      Query Match      66.1%; Score 15.2; DB 19; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 CANANNCCKRAASMANCCNRSYTC 23
      ||||||||||||||||||
Db      1 CANANNCCKRAASMANCCNRSYTC 23

RESULT 2
AAS19699
ID      AAS19699 standard; DNA; 23 BP.
XX
XX      AAS19699;
XX
XX      09-APR-2002 (first entry)
XX
XX      PCR primer #2 used to amplify DNA fragment of geranium PHSacc genes.
XX
XX      Geranium; 1-aminocyclopropane-1-carboxylate synthase gene promoter;
XX      ACC synthase; plant transcription regulation; plant; PCR; primer;
XX      gPHSacc49; ss.
XX
XX      pelargonium x hortorum.
XX
XX      WO200185754-A1.
XX
XX      15-NOV-2001.
XX
XX      09-MAY-2001; 2001WO-US15023.
XX
XX      09-MAY-2000; 2000US-203021P.
XX      12-OCT-2000; 2000US-239782P.
XX
XX      (COLS ) UNIV COLORADO STATE.
XX      (TAGA-) TAGAWA GREENHOUSES INC.
XX

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PI      Ranu RS:
XX
XX      WPI; 2002-075241/10.
XX
XX      New promoter from the 1-aminocyclopropane-1-carboxylate synthase gene
XX      of geranium, useful to regulate level of transcription of coding
XX      sequence in geranium and other plants -
XX
XX      Claim 7; Fig 2; 38pp; English.
XX
XX      The present invention relates to the isolation of promoter DNA from
XX      geranium (pelargonium x hortorum) genomic clone gPHSacc49 (gPHSacc49).
XX      This promoter represents the ACC (1-aminocyclopropane-1-carboxylate)
XX      synthase gene promoter. The promoter is useful to regulate the
XX      transcription level of a coding sequence in geranium and other plants.
XX      The present sequence represents a PCR primer used to amplify a DNA
XX      fragment of geranium PHSacc genes.
XX
XX      Sequence 23 BP; 5 A; 5 C; 0 G; 1 T; 12 other:
XX
XX      Query Match      66.1%; Score 15.2; DB 24; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 CANANNCCKRAASMANCCNRSYTC 23
      ||||||||||||||||||
Db      1 CANANNCCKRAASMANCCNRSYTC 23

RESULT 3
ABQ65439
ID      ABQ65439 standard; DNA; 748 BP.
XX
XX      ABQ65439;
XX
XX      21-AUG-2002 (first entry)
XX
XX      Arabidopsis thaliana polynucleotide seq ID NO 16.
XX
XX      Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
XX      stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
XX      insecticide; antibiotic; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      US2002059663-A1.
XX
XX      16-MAY-2002.
XX
XX      26-JAN-2001; 2001US-0770149.
XX
XX      27-JAN-2000; 2000US-178506P.
XX
XX      (GORL/) GORLACH J.
XX      (ANY/) AN Y.
XX      (HANT/) HAMILTON C M.
XX      (PRIC/) PRICE J L.
XX      (RAIN/) RAINES T M.
XX      (YUY/) YU Y.
XX      (RAME/) RAMEAKA J G.
XX      (PAGE/) PAGE A.
XX      (MATH/) MATHEW A V.
XX      (LEDF/) LEDFORD B L.
XX      (WOES/) WOESSNER J P.
XX      (HAAS/) HAAS W D.
XX      (GARC/) GARCIA C A.
XX      (KRIC/) KRICKER M.
XX      (SLAT/) SLATER T.
XX      (DAVI/) DAVIS K R.
XX      (ALLE/) ALLEN K.
XX      (HOFF/) HOFFMAN N.
XX      (HURE/) HURBAN P.
XX

```

PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaux JG, Puga A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Krieger M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 DR WPI: 2002-4792;4/51.
 XX
 XX
 PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
 PT useful e.g. for preparing transgenic plants with increased resistance
 PT or altered metabolism
 PS
 XX Claim 1: SEQ ID NO 16; 40pp + Sequence Listing; English.
 CC The invention relates to nucleic acids (I) that hybridise under stringent
 CC conditions to any of 999 sequences (AB05424-AB06422) or their
 CC fragments (I) are used to express the corresponding polypeptides (II) or
 CC to produce genetically modified plant cells or transgenic plants, which
 CC may have improved resistance to disease or stress, or altered
 CC metabolic/biosynthetic pathways (for production of commercial,
 CC nutritional or medicinal products), or generally any trait of interest,
 CC or can be used to screen for biologically active agents (e.g. fungicides,
 CC insecticides and antibiotics).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docID=999909770149.
 CC
 SQ Sequence 748 BF: 209 A; 202 C; 120 G; 213 T; 4 other;
 Query Match 66.1%; Score 15.2; DB 24; Length 748;
 Best Local Similarity 47.8%; Pred. No. 2.8e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANNCRAAAMCNCNRSYTC 23
 DB 217 CAACCCCTAAACCATCGACCTC 239
 ID AAT38897 standard; cDNA; 1087 BP.
 AC AAT38897;
 XX
 XX 10-FEB-1997 (first entry)
 DE Carnation ACC synthase gene fragment.
 XX
 XX Carnation: 1-aminocyclopentane-1-carboxylic acid synthase;
 KM ACC synthase; co-suppression; ethylene; senescence;
 KM transgenic plant; ss.
 XX
 XX Dianthus sp. cv. White Sin.
 OS
 PN W09635792-A1.
 XX
 PD 14-NOV-1996.
 XX
 PF 09-MAY-1996; 36MO-AU00286.
 XX
 PR 09-MAY-1995; 35AU-0002862.
 XX
 PA (ALLR-) ALLRAD NO 1 PTY LTD.
 PA (FLOR-) FLORIGENE INVESTMENTS PTY LTD.
 XX
 PI Cornish EC, Graham MW, Guttererson NI, Michael MZ;
 PI Tucker WT;
 XX
 XX WPI: 1996-51868/51.
 DR P-PSDB: AAW0455).
 XX
 PT Producing transgenic plants, with reduced climacteric ethylene
 PT prodn. - to give flowers and buds, specifically carnations, with
 PT increased post-harvest life

XX
 PS Claim 10: Page 42-44; 98pp; English.
 XX
 XX A non full-length gene (AAT38897) comprises nucleotides 287-1373 of
 CC a 1-aminocyclopentane-1-carboxylic acid (ACC) synthase gene
 CC (AAT38896) isolated from carnation cv. White Sin. It was obtd. by
 CC PCR amplification of carnation cDNA using primers (AAT38899-900)
 CC based on highly conserved regions of the ACC synthase gene.
 CC Transgenic carnation plants carrying the non full-length gene show
 CC reduced prodn. of ACC synthase or ACC synthase-specific mRNA as a
 CC result of co-suppression. This leads to decreased climacteric
 CC ethylene prodn. by the plant and hence delayed senescence of
 CC flowers and buds after cutting, and increased post-harvest life.
 CC
 SQ Sequence 1087 BF: 309 A; 204 C; 251 G; 323 T; 0 other;
 Query Match 66.1%; Score 15.2; DB 17; Length 1087;
 Best Local Similarity 47.8%; Pred. No. 3e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANNCRAAAMCNCNRSYTC 23
 DB 1085 CAACCCCTAAACCATCGACCTC 1063
 ID AAT72631/C
 XX AAT72631 standard; DNA; 1096 BP.
 AC AAT72631;
 XX
 XX 27-JAN-1998 (first entry)
 DE Mangifera indica ACC synthase miaccl gene.
 XX
 XX Mangifera indica ACC synthase miaccl gene.
 KM ACC synthase; S-adenosyl-L-methionine methylthiodenosine lyase;
 KM miaccl; ethylene biosynthesis; transgenic plant; senescence;
 KM antisense expression system; plant development; fruit ripening;
 KM EC 4.4.1.14; mango; multigene family; ss.
 XX
 OS Mangifera indica.
 XX
 FH Key Location/Qualifiers
 FT 1..1096
 FT CDS
 FT /*tag= 3
 FT /product= miaccl
 FT /EC_number= 4.4.1.14
 FT /note= "Sequence represents 75% of the coding
 FT sequence and does not contain the start
 FT or stop codons."
 FT
 PN W09711166-A1.
 XX
 PD 27-MAR-1997.
 XX
 PF 20-SEP-1996; 96MO-AU00591.
 XX
 PR 02-MAY-1996; 96AU-0009603.
 XX
 PR 20-SEP-1995; 95AU-0005559.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA
 XX Botella JR;
 PI
 XX WPI: 1997-202875/18.
 DR P-PSDB: AAW18289.
 XX
 XX Pineapple, papaya and mango ACC synthase genes - used in gene
 PT therapy to produce fruits with reduced senescence
 PS Claim 4: Fig 4; 46pp; English.
 XX
 XX This sequence represents a novel gene, miaccl, which is a member

CC of an ACC synthase multigene family found in mango. ACC synthase is
CC involved in the pathway for ethylene biosynthesis and the rate of
CC endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.
XX
SQ Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;
Query Match 66.1%; Score 15.2; DB 18; Length 1096;
Best Local Similarity 47.8%; Pred. No. 3e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
OY 1 CANANCKRASMNCNRSYTC 23
DB 1088 CAGACTCTGAACCAACGAGCTC 1066
|||1::||:|1|::|1|
RESULT 6
AAT72630/C
ID AAT72630 standard; DNA; 1098 BP.
XX
AC AAT72630;
XX
DT 27-JAN-1998 (first entry)
XX
DE Carica papaya ACC synthase capacc2 gene.
XX
KW ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KW capacc2; ethylene biosynthesis; transgenic plant; senescence;
KW antisense expression system; plant development; fruit ripening;
KW EC 4.4.1.14; papaya; multigene family; ss.
XX
OS Carica papaya.
XX
FH Key Location/Qualifiers
FT CDS 1..1098
FT /*tag= a
FT /EC_number= 4.4.1.14
FT /product= capacc2
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."
XX
XX
XX W09711166-A1.
XX
XX
XX 27-MAR-1997.
XX
XX
XX 20-SEP-1996; 96MO-AU00591.
XX
XX
XX 02-MAY-1996; 96AU-0009603.
XX 20-SEP-1995; 95AU-0005559.
XX
XX
XX (UYOU) UNIV QUEENSLAND.
XX
XX
XX Botella JR.
XX
XX WPI: 1997-202875/18.
XX P-PSDB: AAW18288.
XX
XX
XX Pineapple, papaya and mango ACC synthase genes - used in gene
XX therapy to produce fruits with reduced senescence
XX
XX
XX Claim 3; Fig 3; 46pp; English.
XX
XX This sequence represents a novel gene, capacc2, which is a member
XX of the ACC synthase multigene family found in papaya. The enzyme ACC
XX synthase is involved in the pathway for ethylene biosynthesis and the
XX rate of endogenous expression of ACC synthase is considered to limit

CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.
XX
SQ Sequence 1098 BP; 276 A; 275 C; 299 G; 248 T; 0 other;
Query Match 66.1%; Score 15.2; DB 18; Length 1098;
Best Local Similarity 47.8%; Pred. No. 3e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
OY 1 CANANCKRASMNCNRSYTC 23
DB 1091 CATACTCTGAACCAACCGGCTC 1069
|||1::||:|1|::|1|
RESULT 7
AAT72629/C
ID AAT72629 standard; DNA; 1104 BP.
XX
AC AAT72629;
XX
DT 27-JAN-1998 (first entry)
XX
DE Carica papaya ACC synthase capacc1 gene.
XX
XX
KW ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KW capacc1; ethylene biosynthesis; transgenic plant; senescence;
KW antisense expression system; plant development; fruit ripening;
KW EC 4.4.1.14; papaya; multigene family; ss.
XX
OS Carica papaya.
XX
FH Key Location/Qualifiers
FT CDS 1..1104
FT /*tag= a
FT /EC_number= 4.4.1.14
FT /product= capacc1
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."
XX
XX
XX W09711166-A1.
XX
XX
XX 27-MAR-1997.
XX
XX
XX 20-SEP-1996; 96MO-AU00591.
XX
XX
XX 02-MAY-1996; 96AU-0009603.
XX 20-SEP-1995; 95AU-0005559.
XX
XX
XX (UYOU) UNIV QUEENSLAND.
XX
XX
XX Botella JR.
XX
XX WPI: 1997-202875/18.
XX P-PSDB: AAW18287.
XX
XX
XX Pineapple, papaya and mango ACC synthase genes - used in gene
XX therapy to produce fruits with reduced senescence
XX
XX
XX Claim 2; Fig 2; 46pp; English.
XX
XX This sequence represents a novel gene, capacc1, a member of the papaya
XX ACC synthase multigene family. ACC synthase is an enzyme involved in
XX the pathway for ethylene biosynthesis and the rate of endogenous
XX expression of ACC synthase is considered to limit substantially the rate
XX of ethylene production. Endogenous ethylene is often deleterious to
XX crops, especially if some form of mechanical wounding has occurred and
XX diminishes their post harvest quality and storage life. Novel ACC

CC synthase genes expressed in transgenic plants using either sense or
CC antisense expression system may be used to control the regulation of
CC plant development, in particular fruit ripening, reducing senescence and
CC thus improving storage life.
XX
SQ Sequence 1104 BP; 325 A; 214 C; 257 G; 308 T; 0 other;
Query Match 66.1%; Score 15.2; DB 18; Length 1104;
Best Local Similarity 47.8%; Pred. No. 3e+02; Mismatches 11; Conservative 7; Indels 0; Gaps 0;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCNRSTYC 23
DB 1097 CAGACGCTGACAGCAGGATTC 1075
RESULT 8
AAH77094/C
ID AAH77094 standard; cDNA; 1154 BP.
XX
AC AAH77094;
XX
DT 15-DEC-2001 (first entry)
XX
DE Human ATP-dependent serine proteinase 31-encoding cDNA.
XX
KW Human; ATP-dependent serine proteinase 31; recombinant production;
KW malignant tumor; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytosolic; anti-HIV; antiinflammatory; immunomodulator; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 128..985
FT /aaq= a
FT /product= "Human ATP-dependent serine proteinase 31"
XX
XX MO200175125-A1.
XX
PD 11-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-CN00405.
XX
PR 24-MAR-2000; 2000CN-0115085.
XX
PA (SHAN-) SHANGHAI BIOWINDON GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
PI MPI: 2001-626440/72.
XX
DR P-PSDB; AAG66837.
XX
XX Human adenosine triphosphate dependent serine proteinase 31 and encoded
PT polynucleotide, applicable in diagnosis and treatment of malignant
PT tumor, hemopathy, human immunodeficiency virus infection, immunological
PT diseases and inflammation -
XX
PS Claim 6; Page 33-31; 36pp; Chinese.
XX
CC This sequence represents cDNA encoding human ATP-dependent serine
CC proteinase 31. The protein has a molecular weight of 31 kD. The invention
CC relates to human ATP-dependent serine proteinase 31 (AAG66837), nucleic
CC acids encoding it (AAH77094), and a method for the recombinant production
CC of ATP-dependent serine proteinase 31. The present invention additionally
CC discloses an antagonist of ATP-dependent serine proteinase 31 for
CC therapeutic use, and an antibody which specifically binds to ATP-
CC dependent serine proteinase 31. ATP-dependent serine proteinase 31, and
CC nucleotides which encode it may be used for treating a variety of
CC diseases, such as malignant tumours, blood diseases, HIV (human
CC immunodeficiency virus) infection, immune disorders and inflammatory
CC conditions. The protein may also be used to screen for modulators of its
CC activity or for peptide fingerprinting identification. The polynucleotide

CC can be used as a primer for nucleic acid amplification reactions or as a
CC probe for hybridisation reactions, or in producing gene chips or
CC microarrays.
XX
SQ Sequence 1154 BP; 302 A; 228 C; 290 G; 334 T; 0 other;
Query Match 66.1%; Score 15.2; DB 22; Length 1154;
Best Local Similarity 47.8%; Pred. No. 3e+02; Mismatches 11; Conservative 7; Indels 0; Gaps 0;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCNRSTYC 23
DB 174 CAGAGACGGAAGCAGCAAGCTC 152
RESULT 9
AAT66247/C
ID AAT66247 standard; DNA; 1170 BP.
XX
AC AAT66247;
XX
DT 28-JUL-1997 (first entry)
XX
DE ACC synthase GAC-2 DNA.
XX
KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; antisense;
KW ethylene; transgenic plant; petargonium x domesticum;
KW in vitro propagation; tissue culture; ripening; ss.
XX
OS Not identified.
XX
PN WO9717429-A1.
XX
PD 15-MAY-1997.
XX
PE 08-NOV-1996; 96WO-US17954.
XX
PR 09-NOV-1995; 95US-0555755.
XX
PA (OGLE-) OGLEVEE LTD.
XX
PA (PENN-) PENN STATE RES FOUND.
XX
PI Arteca J, Arteca RN, Oglevee-O'Donovan W, Stoots E;
XX
DR WPI: 1997-281019/25.
XX
DR P-PSDB; AAM09879.
XX
XX Commercial propagation of transgenic plants by tissue culture -
PT especially Petargonium x domesticum with decreased ethylene
PT formation
XX
PS Claim 14; Page 24; 36pp; English.
XX
CC 2 DNA sequences (AAT66246-47) respectively code for
CC 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1
CC (AAM09878) and GAC-2 (AAM09879), enzymes involved in the biosynthesis
CC of ethylene in plants. In a method for the commercial production
CC of transgenic plants, Agrobacterium vectors carrying antisense
CC genes for ACC synthase or ACC oxidase (see also AAT66248) are used
CC to inoculate petiole explants of a mother plant, pref.
CC Petargonium x domesticum. The resulting callus is cultured and
CC used to regenerate transgenic plants. The antisense genes prevent
CC ACC synthase or ACC oxidase expression and hence ethylene
CC formation and fruit ripening.
XX
SQ Sequence 1170 BP; 319 A; 263 C; 297 G; 291 T; 0 other;
Query Match 66.1%; Score 15.2; DB 18; Length 1170;
Best Local Similarity 47.8%; Pred. No. 3e+02; Mismatches 11; Conservative 7; Indels 0; Gaps 0;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCNRSTYC 23

PD 03-MAR-1998.
 XX
 PF 07-JUN-1995; 95US-0481171.
 XX
 PR 02-APR-1992; 92US-0862493.
 XX 10-SEP-1990; 90US-0579896.
 PR 25-JAN-1995; 95US-0378313.
 PR 07-JUN-1995; 95US-0481171.
 XX
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Sato T, Theologis A;
 XX WPI: 1998-2060C5/18.
 DR P-PSDB; AAW47310;
 XX
 PT DNA encoding anti-sense RNA blocking plant ACC synthase expression -
 XX is used for producing transgenic plants with delayed fruit ripening -
 XX Example 1; Columns 33-38; 91pp; English.
 XX
 CC The present sequence is the zucchini
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase clone PACCl.
 CC PACCl was used in the isolation of conserved sequences from five
 CC tomato LE-ACC 1a, LE-ACC 1b, LE-ACC 2, LE-ACC 3, and LE-ACC 4) and two
 CC zucchini (CP-ACC 1a and CP-ACC 1b) ACC synthases.
 CC A novel DNA molecule comprises an expression system which, when
 CC complemented in a plant host cell, generates RNA that is sufficiently
 CC complementary to an RNA transcript of an endogenous ACC synthase
 CC gene to prevent its synthesis. The expression system consists of
 CC the reverse transcript of the antisense RNA (i.e. cDNA) operably
 CC linked to control sequences that effect its transcription into the
 CC ACC synthase gene by primer pairs encoding conserved ACC synthase
 CC sequences. The DNA molecule can be used to delay ripening of
 CC tomato or zucchini fruits.
 CC
 SQ Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
 XX
 Query Match 66.1%; Score 15.2; DB 19; Length 1703;
 Best Local Similarity 47.8%; Pred. No. 3.2e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANNCRAASMANCCRSYTC 23
 DB 1254 CAACCTCGAATCPAACCTCGCTC 1232
 XX
 RESULT 13
 AAD04541/C
 ID AAD04541 standard; cDNA; 1703 BP.
 XX
 AC AAD04541;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Zucchini 1-aminocyclopropane-1-carboxylic acid synthase (PACCl) cDNA.
 XX
 KW Zucchini; 1-aminocyclopropane-1-carboxylic acid synthase; PACCl;
 XX ethylene production; fruit ripening; transgenic plant; ss.
 XX
 OS Cucurbita pepo.
 XX
 FH Key Location/Qualifiers
 FT 11..1492
 FT //tag="a" "Zucchini PACCl"
 FT //product="Zucchini PACCl"
 XX
 XX US6207881-B1.
 XX 27-MAR-2001.
 XX
 XX 25-JAN-1995; 55US-0378313.

XX 19-APR-1992; 92US-0862493.
 PR 10-SEP-1990; 90US-0579896.
 XX
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Theologis A, Sato T;
 XX WPI: 2001-289591/30.
 DR P-PSDB; AAE00980.
 XX
 PT Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic
 PT acid synthase, LE-ACC2 useful for producing ACC synthase which is
 PT essential for the production of ethylene in higher plants
 XX
 PS Example 1; Fig 1B; 92pp; English.
 XX
 CC The present sequence is a cDNA encoding zucchini (Cucurbita pepo)
 CC 1-aminocyclopropane-1-carboxylic acid synthase (PACCl). ACC synthase are
 CC capable of catalysing the conversion of Adomet (S-adenosyl methionine)
 CC to ACC and methyl thiodenosine (MTA). ACC DNA is useful for producing
 CC ACC synthase which is essential for the production of ethylene in higher
 CC plants, where ethylene is a determinant of fruit ripening. The ACC DNA
 CC is also useful for producing transgenic plants which are overproducers
 CC of or are deficient in ACC synthase.
 XX
 SQ Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
 XX
 Query Match 66.1%; Score 15.2; DB 22; Length 1703;
 Best Local Similarity 47.8%; Pred. No. 3.2e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANNCRAASMANCCRSYTC 23
 DB 1254 CAACCTCGAATCPAACCTCGCTC 1232
 XX
 RESULT 14
 AAF23618/C
 ID AAF23618 standard; DNA; 1703 BP.
 XX
 AC AAF23618;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Zucchini ACC synthase clone PACCl coding sequence.
 XX
 KW ACC synthase; 1-aminocyclopropane-1-carboxylic acid synthase;
 XX ethylene production; fruit ripening; enzyme; zucchini; ss.
 XX
 OS Cucurbita pepo.
 XX
 PN US6156956-A.
 XX
 PD 05-DEC-2000.
 XX
 DE 02-MAR-1998; 98US-0033349.
 XX
 PF 25-JAN-1995; 95US-0378313.
 PR 02-APR-1992; 92US-0862493.
 PR 07-JUN-1995; 95US-0481171.
 PR 10-SEP-1990; 90US-0579896.
 XX
 PA (USDA) US DEPT OF AGRICULTURE.
 XX
 PI Sato T, Theologis A;
 XX WPI: 2001-079558/09.
 DR P-PSDB; AAB59716.
 XX
 PT Expression cassette for producing transgenic plants exhibiting
 PT inhibited ethylene production and delayed fruit ripening, comprises
 PT complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid

```

PT synthase synthesis
XX
PS Example 1: Fig 1; 91pp; English.
XX
CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for the
CC production of ethylene in higher plants; ethylene is a determinant of
CC fruit ripening. The present invention relates to an expression cassette
CC which comprises the reverse transcript of RNA complementary to an RNA
CC transcribed from ACC synthase gene. The expression cassette can be used
CC to prevent ACC gene expression. The expression cassette is useful for
CC inhibiting ethylene production and fruit ripening, when introduced into a
CC plant or plant cells. The present sequence is the coding sequence for
CC zucchini ACC synthase clone PAC01.
XX
SQ Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;

Query Match      66.1%; Score 15.2; DB 22; Length 1703;
Best Local Similarity 47.8%; Pred. No. 3.2e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMAMCNRSTYC 23
   ||| 1::1::1 ||| 1::1::1
DB 1254 CAACTCGAACAACCACTGCGCTC 1232

RESULT 15
AAX27501/C
ID AAX27501 standard; cDNA; 1712 BP.
XX
AC AAX27501;
XX
DT 26-MAY-1999 (first entry)
XX
DE Banana 1-aminocyclopropane-1-carboxylic acid synthase (ACS) cDNA.
XX
KM 1-aminocyclopropane-1-carboxylic acid synthase; ACS; EFE; banana;
KM ethylene forming enzyme; ethylene biosynthesis; plant; fruit ripening;
KM transgenic; enzyme; inhibition; flavour; texture; ss.
XX
OS Musa sp.
XX
PN US5886164-A.
XX
PD 23-MAR-1999.
XX
PF 15-APR-1996; 96US-0632598.
XX
PR 15-APR-1996; 96US-0632598.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Bird CR, Fletcher JD;
XX
DR WPI: 1999-228611/19.
XX
PT Novel isolated cDNA molecules ((PASC6) and (PAC07)) encoding
PT 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene
PT forming enzyme (EFE) - useful for modifying fruit ripening
PT characteristics, especially in bananas
XX
PS Claim 1; Columns 11-14; 22pp; English.
XX
XX The invention relates to two isolated cDNA molecules ((PASC6) and
CC (PAC07)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS)
CC and an ethylene forming enzyme (EFE), respectively. The clones are
CC deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814,
CC respectively. PASC6 and PAC07 may be used to genetically control
CC ethylene biosynthesis in plants and hence regulate the ethylene-induced
CC processes involved in fruit ripening (and other ethylene related
CC processes). Vectors comprising the cDNA sequences may be used to produce
CC transgenic bananas with altered fruit ripening characteristics. The
CC orientation of the PASC6 and PAC07 used in the construct, will determine
CC how the ripening process is affected. If the genes have a sense

```

```

CC orientation, and transcribe mRNA that encodes an active enzyme. The rate
CC of ripening will be increased (up-regulation) (however, full-length sense
CC constructs can also be used to inhibit enzyme expression by co-
CC inhibition). If genes encode antisense mRNA, they will inhibit the
CC expression of the genes involved in fruit ripening and hence slow the
CC process down (down-regulation). In this manner different spatial and
CC temporal patterns of genes expression can be produced. Retardation of the
CC rate of ripening will reduce the rate of deterioration of banana fruit
CC after harvest. This helps in production of high quality fruit that has
CC improved flavour and texture. The present sequence represents the cDNA
CC sequence of the banana ACS enzyme.
XX
SQ Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

Query Match      66.1%; Score 15.2; DB 20; Length 1712;
Best Local Similarity 47.8%; Pred. No. 3.2e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMAMCNRSTYC 23
   ||| 1::1::1 ||| 1::1::1
DB 1265 CACACCCCTGACACCCCGCGCTC 1243

```

Search completed: March 10, 2003, 05:25:16
Job time : 173.5 secs

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 04:48:25 ; Search time 957.5 Seconds

(without alignments)
699.075 Million cell updates/sec

Title: US-09-975-842-2

Perfect score: 23

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Scoring table:

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Searched: 205640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GerEmbl:*

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_ov:*

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12: gb_ov:*

13: gb_ov:*

14: gb_ov:*

15: gb_ov:*

16: gb_ov:*

17: gb_ov:*

18: gb_ov:*

19: gb_ov:*

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21: gb_ov:*

22: gb_ov:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	67.0	23	AR050170	AR050170 Sequence
2	15.4	67.0	219	TOMACCD	M83329 Lycopersico
3	15.4	67.0	221	LEU18058	U18058 Lycopersico
4	15.4	67.0	265	AB005723	AB005723 Actinidia
5	15.4	67.0	265	AF146027	AF146027 Actinidia
6	15.4	67.0	268	AF146026	AF146026 Actinidia
7	15.4	67.0	268	TOMACCA	M83318 Lycopersico
8	15.4	67.0	271	AB005722	AB005722 Actinidia
9	15.4	67.0	271	AF146025	AF146025 Actinidia
10	15.4	67.0	271	TOMACCA	M83320 Lycopersico
11	15.4	67.0	271	PSACS2	X83105 P. sativum m
12	15.4	67.0	273	PSACS2	U74458 Lycopersico
13	15.4	67.0	308	LEACSLA1	U74460 Lycopersico
14	15.4	67.0	308	LEACSLA1	U74461 Lycopersico
15	15.4	67.0	314	FSY420187	AF090351 Striga he
16	15.4	67.0	317	AF090351	AJ420186 Fagus syl
17	15.4	67.0	318	FSY420186	U17974 Lycopersico
18	15.4	67.0	721	LEU17974	AF048753 Citrus X
19	15.4	67.0	723	OSACCA5	227242 O. sativa (P
20	15.4	67.0	735	OSACCA5	U86865 Actinidia
21	15.4	67.0	743	ACU86865	AF074932 Sinapis a
22	15.4	67.0	757	AF074932	U35778 Trilicium ae
23	15.4	67.0	779	TAU35778	AF074931 Sinapis a
24	15.4	67.0	940	AF074931	AJ420188 Fagus syl
25	15.4	67.0	941	FSY420188	AF053355 Phaseolus
26	15.4	67.0	956	AF053355	AF074930 Sinapis a
27	15.4	67.0	960	AF074930	AR135348 Sequence
28	15.4	67.0	961	AR135348	AR135347 Sequence
29	15.4	67.0	966	AR135347	AR093264 Sequence
30	15.4	67.0	994	AR093264	U37819 Helianthus
31	15.4	67.0	1008	CSU59813	U37813 Cucumis sat
32	15.4	67.0	1025	CSU59813	AF074929 Sinapis a
33	15.4	67.0	1027	AF074929	AF074928 Sinapis a
34	15.4	67.0	1041	AF074928	AB015494 Passiflor
35	15.4	67.0	1054	AB015494	AF015495 Passiflor
36	15.4	67.0	1060	AF015495	AF015494 Passiflor
37	15.4	67.0	1080	AF015495	AF015494 Passiflor
38	15.4	67.0	1080	AF015495	AF015494 Passiflor
39	15.4	67.0	1089	AB021907	AB021907 Musa acum
40	15.4	67.0	1089	AB021907	AB021907 Musa acum
41	15.4	67.0	1089	CAACCI	X82265 C. annuum mRN
42	15.4	67.0	1092	AF083814	AF083814 Antirrhin
43	15.4	67.0	1094	AF518327	AF518327 Populus t
44	15.4	67.0	1094	MDU73815	U73815 Malus domes
45	15.4	67.0	1096	MTU22523	U22523 Mangifera l

ALIGNMENTS

RESULT 1

AR050170

LOCUS AR050170

DEFINITION Sequence 9 from patent US 5824875.

ACCESSION AR050170

VERSION AR050170.1

KEYWORDS GI:5972162

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 23)

AUTHORS Renu, R.S.

TITLE 1-aminocyclopropane-1-carboxylate synthase genes from pelargonium

JOURNAL Patent: US 5824875-A 9 20-Oct-1998;

FEATURES Location/Qualifiers

source	1. .23	/organism="unknown"
BASE COUNT	0 a 2 c 7 g 4 t 10 others	
ORIGIN		
Query Match	67.0%; Score 15.4; DB 6; Length 23;	
Best Local Similarity	100.0%; Pred. No. 2.1e+03;	
Matches 23; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GGNATNCNGGNTTYMGNTNGG 23	
Db	1 GGNATNCNGGNTTYMGNTNGG 23	
RESULT 2		
TOMACCD	219 bp	linear
LOCUS	PLN 19-JUN-1995	
DEFINITION	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate homologue	
ACCESSION	M83329	
VERSION	GI:170510	
KEYWORDS	1-aminocyclopropane-1-carboxylate synthase; homologue.	
SOURCE	Lycopersicon esculentum ripe pericarp CDNA to mRNA.	
ORGANISM	Lycopersicon esculentum	
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.	
AUTHORS	1 (bases 1 to 219)	
TITLE	Yip,W.K., Moore,T. and Yang,S.F.	
JOURNAL	Differential accumulation of transcripts for four tomato	
MEDLINE	1-aminocyclopropane-1-carboxylate synthase homologs under various	
PUBMED	conditions	
FEATURES	Procc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)	
source	1549612	
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	1. .219	
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	/dev_stage="ripe"	
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	/EC_number="4.4.1.14"	
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	/codon_start=1	
	/product="1-aminocyclopropane-1-carboxylate synthase"	
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	/db_xref="GI:867993"	
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BASE COUNT	67 a 38 c 41 g 73 t	
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Query Match	67.0%; Score 15.4; DB 8; Length 219;	
Best Local Similarity	56.5%; Pred. No. 1.1e+03;	
Matches 13; Conservative	4; Mismatches 6; Indels 0; Gaps 0;	
QY	1 GGNATNCNGGNTTYMGNTNGG 23	
	: : : : : : : :	
Db	151 GGTTCACAGGATTCAGAGTG 173	
RESULT 3		
LOCUS	LEU18058	221 bp
DEFINITION	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase	
ACCESSION	(LE-ACS5) DNA, partial cds.	
VERSION	U18058	
KEYWORDS	U18058.1 GI:1561701	
SOURCE	Lycopersicon esculentum.	
ORGANISM	Lycopersicon esculentum	

REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I: Solanales: Solanaceae: Solanum: Lycopersicon.			
AUTHORS	1 (bases 1 to 221)			
TITLE	Krawakita,K., Hennig,L., Lincoln,J.E., Rottmann,W.H., Campbell,A.D., Zaremboinski,T.J., Yu,G.X., Taylor,L.D. and Theologis,A. The tomato 1-aminocyclopropane-1-carboxylate (ACC) synthase multigene family is encoded by at least eight members			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 221)			
AUTHORS	Theologis,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-DEC-1994) Athanasios Theologis, Plant Gene Expression Center, ARS/USDA, 800 Buchanan Street, Albany, CA 94710 and Department of Plant Biology, University of California, Berkeley, CA 94720, USA			
FEATURES	Location/Qualifiers			
SOURCE	1..221			
	/organism="Lycopersicon esculentum"			
	/cultivar="Rutgers"			
	/db_xref="taxon:4081"			
	/clone="PSEF3 (stock #394)"			
	1..221			
gene	/gene="LE-ACS5"			
	<1..>221			
	/gene="LE-ACS5"			
	/EC_number="4.4.1.14"			
	/function="converts SAM to ACC; plant hormone biosynthesis"			
	/standard_name="Lycopersicon esculentum 1-amino-cyclopropane-1-carboxylate synthase"			
	/note="direct precursor of ethylene; one member of a multigene family; from TZ region to the reaction center; similar to the product encoded by PIR Accession Number C41985"			
	/codon_start=1			
	/product="ACC synthase"			
	/protein_id="AAB48947.1"			
	/db_xref="GI:1561702"			
	/translation="TLITFMFKIHIVSDPEIVAGYFDSPKFEVSIETALDRLEKRS KMNQVHIVSLSSLDLGPGRVGMITSN"			
BASE COUNT	79 a 41 c 40 g 61 t			
ORIGIN	-			
Query Match	67.0% Score 15.4; DB 8; Length 221;			
Best Local Similarity	56.5% Pred. No. 1.6e+03;			
Matches 13; Conservative	4; Mismatches 6; Indels 0; Gaps 0;			
QY	1 GGNATNCNGGNTTATMGNTNGC 23			
	: : :			
Db	181 GGCTTCACAGTTTCAGACTTG 203			
RESULT 4				
AB005723	265 bp mRNA linear PLN 22-JUL-1997			
LOCUS	AB005723			
DEFINITION	Actinidia deliciosa mRNA for ACC synthase, partial cds.			
ACCESSION	AB005723.1 GI:2274792			
VERSION	ACC synthase.			
KEYWORDS	Actinidia deliciosa (sub_species:deliciosa, strain:Hayward)			
SOURCE	wound-treated fruit cDNA to mRNA.			
ORGANISM	Actinidia deliciosa			
	Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Asteridae: Ericales; Actinidiaceae: Actinidia.			
REFERENCE	1 (sites)			
AUTHORS	Ikoma,Y., Yano,M. and Ogawa,K.			
TITLE	Cloning and expression of genes encoding ACC synthase in kiwifruit			
JOURNAL	Acta Horticulturae 398, 179-186 (1995)			
REFERENCE	2 (bases 1 to 265)			
AUTHORS	Ikoma,Y.			

TITLE Direct Submission
JOURNAL Submitted (11-JUL-1997) Yoshinori Ikoma, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu, Shimizu, Shizuoka 424-02, Japan (E-mail: yoshino@okt.affrc.go.jp, Tel: +81-543-69-7111, Fax: +81-543-69-2115)

FEATURES
source
1. .265
/organism="Actinidia deliciosa"
/strain="Hayward"
/sub_species="deliciosa"
/db_xref="taxon:3627"
/tissue_type="wound-treated fruit"
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/codon_start=2
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/protein_id="BA21548.1"
/db_xref="GI:2274793"
/translation="VLDRLIKTVRFNDKNHLYCDEIYAATVFNQPGFISAEII
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CDS
BASE COUNT 78 a 65 c 54 g 68 t
ORIGIN

Query Match 67.0%; Score 15.4; DB 8; Length 265;
Best Local Similarity 56.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTCNCNGNTTYMGNTNGG 23
Db 197 GGCCTCCCTGCGGTTCAGGCTCG 219

RESULT 5
AF146027 265 bp DNA linear PLN 17-MAY-1999
LOCUS Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 2
DEFINITION gene, partial cds.
ACCESSION AF146027
VERSION AF146027.1 GI:4836800
KEYWORDS
SOURCE
ORGANISM
Actinidia chinensis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Actinidaceae; Actinidia.
1 (bases 1 to 265)
XU,C., Chen,K., Chen,D. and Zhang,S.
Molecular cloning of four members of ACC synthase gene family from kiwifruit (Actinidia chinensis Planch.)
Unpublished
2 (bases 1 to 265)
XU,C., Chen,K., Chen,D. and Zhang,S.
Direct Submission
Submitted (27-APR-1999) Department of Horticulture, Huajiaochi Campus, Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang 310029, People's Republic of China
Location/Qualifiers
1. .265
/organism="Actinidia chinensis"
/db_xref="taxon:3625"
/note="Actinidia chinensis Planch"
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/note="ACS2"
/codon_start=3
/product="1-aminocyclopropane-1-carboxylate synthase 2"
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/translation="VLDRLIKTVRFNDKNHLYSDEIYAATVFNKRGFISAEII
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BASE COUNT 81 a 67 c 50 g 67 t
ORIGIN

Query Match 67.0%; Score 15.4; DB 8; Length 265;
Best Local Similarity 56.5%; Pred. No. 1.6e+03;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTCNCNGNTTYMGNTNGG 23
Db 198 GGCCTCCCTGCGGTTCAGGCTCG 220

RESULT 6
AF146026 268 bp DNA linear PLN 17-MAY-1999
LOCUS Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 1b
DEFINITION gene, partial cds.
ACCESSION AF146026
VERSION AF146026.1 GI:4836798
KEYWORDS
SOURCE
ORGANISM
Actinidia chinensis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Actinidaceae; Actinidia.
1 (bases 1 to 268)
XU,C., Chen,K., Chen,D. and Zhang,S.
Molecular cloning of four members of ACC synthase gene family from kiwifruit (Actinidia chinensis Planch.)
Unpublished
2 (bases 1 to 268)
XU,C., Chen,K., Chen,D. and Zhang,S.
Direct Submission
Submitted (27-APR-1999) Department of Horticulture, Huajiaochi Campus, Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang 310029, People's Republic of China
Location/Qualifiers
1. .268
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/db_xref="taxon:3625"
/note="Actinidia chinensis Planch"
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/product="1-aminocyclopropane-1-carboxylate synthase 1b"
/protein_id="AAD30561.1"
/db_xref="GI:4836799"
/translation="TTLRPDLILIFRTSKNHLISDEIYSGTFSSPFSIMEVL
KDSHSPGVNRRVHIVYSKDLGFGFRGIVYSYNDQVTAAT"

CDS
BASE COUNT 63 a 82 c 58 g 65 t
ORIGIN

Query Match 67.0%; Score 15.4; DB 8; Length 268;
Best Local Similarity 56.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTCNCNGNTTYMGNTNGG 23
Db 204 GGCCTCCCGGGGTTCGCGGCTCG 226

RESULT 7
TOMACCA 268 bp mRNA linear PLN 19-JUN-1995
LOCUS Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate homologue
DEFINITION mRNA, partial cds.
ACCESSION M83318
VERSION M83318.1 GI:170505
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids I; Solanales; Solanaceae; Solanum
Lycopersicon
1 (bases 1 to 268)
YIP,W.K., Moore,T. and Yang,S.F.
Differential accumulation of transcripts for four tomato

2
 3
 4
 5
 6
 7

REFERENCE

AUTHORS		Yip,W.K., Moore,T. and Yang,S.F.	
TITLE		Differential accumulation of transcripts for four tomato 1-aminocyclopropane-1-carboxylate synthase homologs under various conditions	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)	
MEDLINE		9219614	
PUBMED		1549612	
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		/db_xref="GI:867991"	
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		DRKREKRWNOVHTVSSISKDGLPGFRVGMKYSNNETLIAATK"	
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ORIGIN		EKMYTFRVENVHTVYSSKIDGLPGFRIGATYSNDENVYSAATK"	
Query Match		67.0%; Score 15.4; DB 8;	
Best Local Similarity		56.5%; Pred. No. 1.6e+03;	
Matches 13; Conservative		4; Mismatches 6; Indels 0; Gaps 0;	
OY		1 GGNATNCNGNTTYMGNTNGG 23	
Db		203 GGCTCCCGGTTTCCGATTGG 225	
RESULT 11		TOMACCG 271 bp mRNA linear PLN 30-JUN-1997	
LOCUS		lycopersicon esculentum 1-aminocyclopropane-carboxylate synthase	
DEFINITION		homologue mRNA, partial cds.	
ACCESSION		M83322	
VERSION		M83322.1 (GI:295351)	
KEYWORDS		Lycopersicon esculentum.	
SOURCE		Lycopersicon esculentum.	
ORGANISM		Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.	
REFERENCE		1 (bases 1 to 271)	
AUTHORS		Yip,W.K., Moore,T. and Yang,S.F.	
TITLE		Differential accumulation of transcripts for four tomato 1-aminocyclopropane-1-carboxylate synthase homologs under various conditions	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)	
MEDLINE		9219614	
PUBMED		1549612	
FEATURES		source	
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BASE COUNT		90 a 61 c 52 g 70 t	
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Query Match		67.0%; Score 15.4; DB 8;	
Best Local Similarity		56.5%; Pred. No. 1.6e+03;	
Matches 13; Conservative		4; Mismatches 6; Indels 0; Gaps 0;	
OY		1 GGNATNCNGNTTYMGNTNGG 23	
Db		205 GGATTCGGGGTGTAGAGTTGG 227	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	SOURCE	SEGMENT	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE
LOCUS LEACSI1	308 bp DNA linear	PLN 16-APR-1997										
DEFINITION	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACSIA) gene, partial cds.											
ACCESSION	U74458											
VERSION	U74458.1	GI:1814255										
KEYWORDS	1 of 2											
ORGANISM	Lycopersicon esculentum											
SOURCE	Lycopersicon esculentum											
SEGMENT	1 of 2											
KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;											
ORGANISM	Lycopersicon											
REFERENCE	1 (bases 1 to 308)											
AUTHORS	Oetiker,J.H., Olson,D.C., Shiu,O.Y. and Yang,S.F.											
TITLE	Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)											
JOURNAL	Plant Mol. Biol. 34 (2), 275-286 (1997)											
MEDLINE	97351561											
PUBMED	9207843											
REFERENCE	2 (bases 1 to 308)											
AUTHORS	Oetiker,J.H., Olson,D.C., Shiu,O.Y. and Yang,S.F.											
TITLE	Direct Submission											
JOURNAL	Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA											
FEATURES	Location/Qualifiers											
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	/product="1-aminocyclopropane-1-carboxylate synthase"											
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	/db_xref="GI:1814258"											
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BASE COUNT	95 a 55 c 63 g 95 t											
ORIGIN												
Query Match	67.0%; Score 15.4; DB 8; Length 308;											
Best Local Similarity	56.5%; Fred. No. 1.6e+03;											
Matches 13; Conservative	4; Mismatches 6; Indels 0; Gaps 0;											
QY	1 GGNATTCGNGGNTTNGATNGG 23											
	: :											
Db	220 GGATTCACGAGTTCAGAGTTGG 242											
RESULT 14												
LEACSI1	308 bp mRNA linear	PLN 16-APR-1997										
LOCUS	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACSIB) mRNA, partial cds.											

FEATURES	source	gene	CDS
JOURNAL MEDLINE PUBMED 97351561 9207843	2 (bases 1 to 308)	Oetliker,J.H., Olson,D.C., Shiu,O.Y. and Yang,S.F. Direct Submission Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA	Location/Qualifiers
REFERENCE AUTHORS TITLE JOURNAL	1..308	/organism="Lycopersicon esculentum"	
FEATURES	1..308	/db_xref="taxon:4081"	
source	/gene="LE-ACS1B"	/gene="LE-ACS1B"	
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	/note="active site region"	/codon_start=1	
	/product="1-aminocyclopropane-1-carboxylate synthase"	/protein_id="AAC9683.1"	
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ORIGIN			
Query Match	67.0%;	Score 15.4;	DB 8; Length 308;
Best Local Similarity	56.5%;	Pred. No. 1.6e+03;	
Matches 13; Conservative	4;	Mismatches 6;	Indels 0; Gaps 0;
OY 1	GGATTCCGCGTTCGTTGCGTTCG 23		
Db 220	GGATTCCGCGTTCGATTTCGATTTCG 242		
RESULT 15			
LEACS6 LOCUS	LEACS6	308 bp	MRNA linear
DEFINITION	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACS6) mRNA, partial cds.		
ACCESSION	U74461		
VERSION	U74461.1		
KEYWORDS	GI:1814265		
SOURCE	Lycopersicon esculentum.		
ORGANISM	Lycopersicon esculentum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
	Lycopersicon.		
	1 (bases 1 to 308)		
REFERENCE	Oetliker,J.H., Olson,D.C., Shiu,O.Y. and Yang,S.F.		
AUTHORS	Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato		
TITLE	(Lycopersicon esculentum)		
	Plant Mol. Biol. 34 (2), 275-286 (1997)		
JOURNAL	9207843		
PUBMED	97351561		
REFERENCE	2 (bases 1 to 308)		
AUTHORS	Oetliker,J.H., Olson,D.C., Shiu,O.Y. and Yang,S.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA		
FEATURES	Location/Qualifiers		
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	/gene="LE-ACS6"		
	<10..>308		

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/gene="LE-ACS6"
/EC_number="4.4.1.14"
/note="stop codon immediately upstream of CDS is an
artifact from the PCR primer sequence; active site region"
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/protein_id="AAC49684.1"
/db_xref="GI:1814266"
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ORIGIN

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Query Match      67.0%; Score 15.4; DB 8; Length 308;
Best Local Similarity 56.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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OY      1 GGNVTNCNGGNTTMMGNRTNGG 23
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Db      220 GGGTTCTCTGCAPTTAGGGTTGG 242

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GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 04:48:25 ; Search time 957.5 seconds

(without alignments)
699.075 Million cell updates/sec

Title: US-09-975-842-3

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	66.1	23	6 AR050171	AR050171 Sequence
2	15.2	66.1	23	6 MS087152	U87152 Musa acumin
3	15.2	66.1	697	8 AF049138	AF049138 Dianthus
4	15.2	66.1	894	8 AF184076	AF184076 Prunus ar
5	15.2	66.1	1089	8 AY061946	AY061946 Rosa hydr
6	15.2	66.1	1089	8 CACAC1	X82265 C. annuum mRN
7	15.2	66.1	1094	8 MDU73815	MDU73815 Malus domes
8	15.2	66.1	1096	8 MIU22523	MIU22523 Mangifera l
9	15.2	66.1	1097	8 AF467782	AF467782 Prunus pe
10	15.2	66.1	1098	8 ATU79524	ATU79524 Arabidopsis
11	15.2	66.1	1098	8 STU70842	STU70842 Solanum tub
12	15.2	66.1	1100	8 AF239989	AF239989 Prunus pe
13	15.2	66.1	1100	8 AF239989	AF239989 Prunus pe
14	15.2	66.1	1100	8 AF239989	AF239989 Prunus pe
15	15.2	66.1	1101	8 AF120898	AF120898 Carica pa
16	15.2	66.1	1104	8 AF184076	AF184076 Prunus ar
17	15.2	66.1	1104	8 VRACCSYN	Z11562 V. radiata m
18	15.2	66.1	1106	8 AF120899	AF120899 Betula pe
19	15.2	66.1	1109	8 AF338652	AF338652 Brassica
20	15.2	66.1	1110	8 D37937	D37937 Cucumis mel
21	15.2	66.1	1113	8 D86241	D86241 Cucumis mel
22	15.2	66.1	1123	8 AF144746	AF144746 Solanum m
23	15.2	66.1	1164	8 AF184077	AF184077 Prunus ar
24	15.2	66.1	1170	8 PHU17231	PHU17231 Pelargonium
25	15.2	66.1	1192	8 AF178077	AF178077 Carica pa
26	15.2	66.1	1194	8 AF178076	AF178076 Carica pa
27	15.2	66.1	1206	8 AF177769	AF177769 Carica pa
28	15.2	66.1	1320	8 AF239663	AF239663 Prunus pe
29	15.2	66.1	1340	8 VRACCSYN4	Z12135 V. radiata g
30	15.2	66.1	1344	8 AF332390	AF332390 Arabidops
31	15.2	66.1	1362	14 AF222638	AF222638 Influenza
32	15.2	66.1	1372	8 MSBACS20E	X96947 Musa acumin
33	15.2	66.1	1383	8 AF332405	AF332405 Arabidops
34	15.2	66.1	1393	8 VRACCSYN5	M94863 Vigna radi
35	15.2	66.1	1393	8 VRACCSYN5	Z12134 V. radiata g
36	15.2	66.1	1394	8 CPA277160	AJ277160 Carica pa
37	15.2	66.1	1400	8 AF312737	AF312737 Malus x d
38	15.2	66.1	1410	8 AF334712	AF334712 Arabidops
39	15.2	66.1	1410	8 LEU17972	LEU17972 Lycopersico
40	15.2	66.1	1413	8 AF332391	AF332391 Arabidops
41	15.2	66.1	1413	8 AF334720	AF334720 Arabidops
42	15.2	66.1	1413	8 AF334720	AF334720 Arabidops
43	15.2	66.1	1425	8 AF332404	AF332404 Arabidops
44	15.2	66.1	1425	8 AF332404	AF332404 Arabidops
45	15.2	66.1	1433	8 CPA277161	AJ277161 Carica pa

ALIGNMENTS

RESULT 1	AR050171	Sequence 10 from patent US 5824875.	23 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR050171					
DEFINITION	AR050171					
ACCESSION	AR050171					
VERSION	AR050171.1	GI:5972163				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 23)					
AUTHORS	Ranu, R.S.					
TITLE	1-aminocyclopropane-1-carboxylate synthase genes from pelargonium					
JOURNAL	Patent: US 5824875-A 10 20-OCT-1998;					
FEATURES	Location/Qualifiers					

source 1. 23
/organism="unknown"

BASE COUNT 5 a 5 c 0 g 1 t 12 others

ORIGIN

Query Match 66.1%; Score 15.2; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
|||||

Db 1 CANANCKRASMNCNRSYTC 23
|||||

RESULT 2
MS087152/c 621 bp mRNA linear PLN 18-FEB-1997

LOCUS MS087152

DEFINITION Musa acuminata 1-aminocyclopropane-1-carboxylate synthase (BACS4)

ACCESSION U87152

VERSION U87152.1 GI:1842048

KEYWORDS

SOURCE Musa acuminata.

ORGANISM Musa acuminata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.

REFERENCE 1 (bases 1 to 621)
AUTHORS Pua, E.-C. and Liu, J.-J.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1997) Department of Biological Sciences, Michigan
Technological University, Houghton, MI 49931, USA

FEATURES
location/Qualifiers
1..621
/organism="Musa acuminata"
/strain="AAA group, cavendish"
/db_xref="taxon:4641"
1..621
/gene="BACS4"
/gene="BACS4"
/EC_number="4.4.1.14"
/note="ACC synthase"
/codon_start=1
/product="1-aminocyclopropane-1-carboxylate synthase"
/protein_id="AAB47554.1"
/db_xref="GI:1842048"
/translation="SNPLGTTMDRETLETLYSYNKKRMHLVCDLFFSGVDPKPSY
SVSEVIEDPDCDRLIHAIISLSKNGVGFVGYISTNDVASCARMSFGLVS
SQOHLASMLGDEFTTSPLATSCARVFTDGLKRVGHICDGNAGLFCWMDL
RPLRLKATVEALELRIMRVINDVKINISRGARFPHCSDEGMPFRCFANM"

BASE COUNT 120 a 169 c 199 g 133 t

ORIGIN

Query Match 66.1%; Score 15.2; DB 8; Length 621;
Best Local Similarity 47.8%; Pred. No. 1.5e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
|||

Db 608 CAGACCGGACACCCGCGCTC 586
|||

RESULT 3
AF049138/c 697 bp mRNA linear PLN 11-MAR-1998

LOCUS AF049138

DEFINITION Dianthus caryophyllus 1-aminocyclopropane-1-carboxylate synthase 2
(ACS2) mRNA, partial cds.

ACCESSION AF049138

VERSION AF049138.1 GI:2947285

KEYWORDS

SOURCE Dianthus caryophyllus.

ORGANISM Dianthus caryophyllus.

REFERENCE
AUTHORS Jones, M.L., Larsen, P.B. and Woodson, W.R.
TITLE Differential expression of three members of the ACC synthase gene
family in carnation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 697)
AUTHORS Jones, M.L., Larsen, P.B. and Woodson, W.R.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) Horticulture and Landscape Architecture,
Purdue University, 1165 Horticulture, West Lafayette, IN
47907-1165, USA

FEATURES
source
1..697
/organism="Dianthus caryophyllus"
/cultivar="white sin"
/db_xref="taxon:3570"
<1..697
/gene="ACS2"
/gene="ACS2"
/note="similar to protein encoded by GenBank Accession
Number X66605"
/codon_start=3
/product="1-aminocyclopropane-1-carboxylate synthase 2"
/protein_id="AAC05377.1"
/db_xref="GI:2947286"
/translation="KRLEPRTFLGLGSLGVGQIQLKSSVGLFVWMDLRHMDPPTVE
GELIMRWIINPKVKNIPSSPCFCHPEPMPFCINMNDMEVALRIRFVLRIR
DVAKPVYASIKRKCMQTNLDRSKNRKDDFKGISDIESPHASNSIASRS"

BASE COUNT 205 a 119 c 166 g 207 t

ORIGIN

Query Match 66.1%; Score 15.2; DB 8; Length 697;
Best Local Similarity 47.8%; Pred. No. 1.5e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
|||

Db 235 CAGACTGTGACACCGCGCTC 213
|||

RESULT 4
AF184076/c 894 bp DNA linear PLN 01-OCT-2000

LOCUS AF184076

DEFINITION Prunus armeniaca ACC synthase (ACS1) gene, partial cds.

ACCESSION AF184076

VERSION AF184076.1 GI:10441264

KEYWORDS

SOURCE Prunus armeniaca.

ORGANISM Prunus armeniaca.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Amygaloideae; Prunus.
1 (bases 1 to 894)
Mbeguile-A-Mbeguile, D. and Fils-Lycaon, B.R.
TITLE Molecular cloning and nucleotide sequence of genomic DNA encoding
ACC synthase from apricot fruit
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 894)
AUTHORS Mbeguile-A-Mbeguile, D. and Fils-Lycaon, B.R.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1999) Station de Technologie des Produits
Vegetaux, Institut National de la Recherche Agronomique,
Agroparc-Domaine Saint Paul, Avignon 84914, France

FEATURES
source
1..894
/organism="Prunus armeniaca"
/db_xref="taxon:36596"
<1..894
/gene="ACS1"

	GENE	CDS	BASE COUNT ORIGIN
mRNA	j0in<1..35,123..>894) /gene="ACS1" /product="ACC synthase" j0in<1..35,123..>894)		
CDS	/note="PA-ACS1" /codon_start=1 /product="ACC synthase" /protein_id="AAG16977.1" /db_xref="GI:10441265" /translation="DAFLVPTPPYDGLDKRDIKMTGVEIITVPCKRADPKPULSTALALLFAFNAKKRGKLVRGRIIISNPSNPVGTSRESILYNLDFAREKNITHISELPFGSIFSEFEVMADIVLEEDLDONRVHIVYLSDLSIPGRACATYSFNKNVTAAKRRLTIRSSISTSOQLISSMSLSDTFKVQRFIDANERLRGMHLKFTTGKGKOLGICICTSNNGFCSMADMGSLIRSYPEKEGELEIMDLDTLVAKVNVTPGSSCHCIEPWRRW"		
BASE COUNT	250 a	177 c	204 g
ORIGIN	177 c	204 g	263 t
Query Match	66.1% Score 15.2; DB 8;	Length 894:	
Best local Similarity	47.8%; Pied No.14e+03;		
Matches	11; Conservative	7; Mismatches	5; Indels
Gaps	0;		
Oy	1 CANANNCKRAA\$MANCCNRSYTC 23		
Dd	:: :: :: :: :: :: 893 CAGACCGGAGACACGGCGGTTC 871		
RESULT 5	Ay061946/c	1089 bp mRNA linear	PLN 30-APR-2002
LOCUS	Ay061946		
DEFINITION	Rosa hybrid cultivar 'Kardinal', 1-aminocyclopropane-1-carboxylate mRNA, partial cds.		
ACCESSION	Ay061946		
VERSION	Ay061946.1		
KEYWORDS	GI:20372647		
ORGANISM	Rosa hybrid cultivar 'Kardinal'.		
SOURCE	Rosa hybrid cultivar 'Kardinal', Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; Magnoliophyta; eudicotyledons; core eudicots; 1 (bases 1 to 1089) Lei,C., Nan,M. and Jumping,G. Cloning of an l-amino;cyclopropane-1-carboxylate cDNA from Rosa cultivar 'Kardinal'. Unpublished		
REFERENCE	2 (bases 1 to 1089) Lei,C., Nan,M. and Jumping,G. Direct Submission Submitted (06-NOV-2001) Ornamental Horticulture and Landscape Architecture, China Agricultural University, No.2 Yuanmingyuan West Road, Beijing 100094, China Location/Qualifiers		
AUTHORS	I..1089		
TITLE	/organism="Rosa hybrid cultivar 'Kardinal'"		
JOURNAL	/cultivar="Kardinal"		
REFERENCE	/db_xref="taxon:180465"		
AUTHORS	/tissue="petals"		
JOURNAL	1..>1089		
FEATURES	/note="ACS"		
SOURCE	/codon_start=1		
	/product="l-aminocyclopropane-1-carboxylate"		
	/protein_id="BAJ34980.1"		
	/db_xref="GI:20372648"		
	/translation="MGLAEMLQSFDVIEMIKRNPRASICTPEGVAFEFNVANFDDYHGPIEDRKALNFMRKSVKVFKPDPDVRYVWAGGATGANETVMFLADPDADFVSPYTAPTRLOLMRTVKRTIVPVGDSSNNFOVTRALEAYEKARNNTNINIGLIITNSPNPIHTVDYRDVLTVLKFIINDKNTHLCVDELTAVTSCPFCTCVTEVIDOVNCNDLFPIHVVISLKDMVGPGLRIGINYNDAYVCARKMSFGISCTOHMISAMLLDNDFVSNLEFFSKRLARRHRFFTTGLEEVGINCLGNAGLYCMMDLRKTLKIQTFEAENV.LWMNIENFKTNVSPSGSFRCVPEGWFRVC"		
	266 c	276 g	263 t
BASE COUNT	284 a	276 g	263 t
ORIGIN			

	Query Match	66.1%	Score 15.2;	DB 8:	length 1089;
	Best Local Similarity	47.8%;	Pred. No. 1.4e+03;		
	Matches 11; Conservative	7;	Mismatches 5;	Indels 0;	Gaps 0;
Oy	1 CANANCKRASMANCNRSTYC 23				
	:: :: :: ::				
Db	1088 CAAACCCGGAGCACGCTGCCTC 1066				
RESULT 6					
LOCUS	CACCI	1089 bp	mRNA	linear	PLN 30-JAN-1995
DEFINITION	C.annum mRNA for 1-aminocyclopropane-1-carboxylate synthase.				
VERSION	X82265.1 GI:642974				
KEYWORDS	1-aminocyclopropane-1-carboxylate synthase; ACC1 gene.				
SOURCE	Capicum annum.				
ORGANISM	Capicum annum				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.					
1 (bases 1 to 1089)					
Harpster,M.H., Howie,W. and Dunsniur,P.					
Unpublished					
2 (bases 1 to 1089)					
Harpster,M.H.					
Direct Submission					
Submitted (20-OCT-1994) M.H. Harpster, DNA Plant Technology Corporation, 6701 San Pablo Avenue, Oakland, California 94608, USA					
JOURNAL	Location/Qualifiers				
TITLE	1..1089				
FEATURES	/organism="Capsicum annum"				
source	/cultivar="VS-300"				
	/db_xref="taxon:4072"				
	/cdate="pbead1.2"				
	/cell_line="VS-300"				
	1..1089				
gene	/gene="ACC1"				
CDs	1..1089				
	/partial				
	/gene="ACC1"				
	/EC_number="4.4.1.14"				
	/codon_start=1				
	/product="1-aminocyclopropane-1-carboxylate synthase"				
	/protein_id="CAA57716.1"				
	/db_xref="GI:642975"				
	/db_xref="SPREPBL:O42655"				
	/translation="MGIAENOLCFDLIOEVMVNNPKASICAKAEDEFOELAFODYH GLPEFROAVAFEMKRGVDRTEDPNILVNSGATGAHEMLAPLADPGDAPLPVPY YPGDRLRMFTGVQLPFPVCESSNDKRVKALEAYEKAAOSNTIKRIILLNPN PLGLDKDTLDIDIVTEINSKNHLVCDELIAATVFQPPPIYSVEVDMSINDLI IHLYSLSKDGLFGPFVGVIYISYNDTVVIDIARKMSEFGLVSTOTOHLLASMSIDEIF LEKIYASSERLSKROGMFTKGIAOVISTLKSNAGLFPMMDLRLLKEPTPDALIEL WRITTHVKLVNSGVSGFSFCSEPMPFRC"				
BASE COUNT	330 a 184 c 245 g 330 t				
ORIGIN					
Query Match	66.1% Score 15.2; DB 8: length 1089;				
Best Local Similarity	47.8%; Pred. No. 1.4e+03;				
Matches 11; Conservative	7; Mismatches 5; Indels 0; Gaps 0;				
Oy	1 CANANCKRASMANCNRSTYC 23				
	:: :: :: ::				
Db	1088 CATACTCGGAGCACTGTGTC 1066				
RESULT 7					
LOCUS	MDU73815	1094 bp	mRNA	linear	PLN 29-AUG-1997
DEFINITION	Malus domestica ACC synthase (MdACS-2) mRNA, partial cds.				
ACCESSION	U73815				
VERSION	. GI:1658059				
KEYWORDS					

SOURCE	Malus x domestica.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE AUTHORS TITLE	1 (bases 1 to 1094) Rosentfield,C.-L., Kiss,E. and Hrazdina,G. MACS-2 (Accession No. U73815) and MdACS-3(Accession No. U73816): two new l-aminocyclopropane-1-carboxylate synthases in ripening apple fruit (PCR96-122)
JOURNAL REFERENCE AUTHORS TITLE	Plant Physiol. 112, 1755 (1996) 2. (bases 1 to 1094) Rosentfield,C.-L., Kiss,E. and Hrazdina,G. Direct Submission Submitted (09-OCT-1996) Food Science & Technology, Cornell University, NYSAES, Geneva, NY 14456, USA
FEATURES	Location/Qualifiers
SOURCE	1..1094 /organism="Malus x domestica" /strain="McIntosh" /db_xref="taxon:3750" /tissue_type="ripening apple fruit"
gene	1..1094 /gene="MdACS-2"
CDS	<1..>1094 /gene="MdACS-2" /EC_number="4.1.1.14" /codon_start=1 /product="ACC synthase" /protein_id="AAB67988.1" /db_xref="GI:1658060" /translation="QMGLAEHQPCFDLLQEMVMNNPKASICTYEAGVDEPDODIAIFODYHGLEPFRKAVARFMEKVGDRGYTFEDPRIVMWSGGATGAHSLEAFCLADPEDADLVTPNYPEFDRLRWRTGVQLFPYVCSSNNFKYTKALEAPYAKQAESNIKYGLIINNSNLPTGIDTKRETLDKIREFINDKNHLVCEDEIYATALCQSPFISISEVMNEVGCNDLVHIYVISXKDIGPFGRVGIIYYNVVNVIARKMSFGSVSTOTRLLIASMSDITIVFNPIKSAMKLISORDHDLFTKGGOVEITTIKSNAGLIPLIMDLRRLETNSTFDEELKLWHIIRNKVLNLSVPGCSFHCSPEGMWRVC"
BASE COUNT	357 a 171 c 229 g 337 t
ORIGIN	
Query Match	66.1%; Score 15.2; DB 8; Length 1094;
Best Local Similarity	47.8%; Pred. No. 1.4e+03;
Matches	11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Oy	1 CANANNCKRASMANCCNRSYTC 23 ::: :: :: Db 1091 CATACCCGGAGCAACTCGCTC 1069
RESULT 8	
MU022523/c	1096 bp mRNA linear PLN 01-JAN-1996
LOCUS	
DEFINITION	Mangifera indica l-aminocyclopropane-carboxylate synthase mRNA, partial cds.
ACCESSION	MU022523
VERSION	U22523
KEYWORDS	U22523.1 GI:1143811
ORGANISM	Mangifera indica.
SOURCE	Mangifera indica
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Anacardiaceae; Mangifera.
AUTHORS	1 (bases 1 to 1096) Botella,J.R.
TITLE	Ethylene evolution and ACC synthase gene expression during ripening of mango fruits
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1096) Botella,J.R.
AUTHORS	Direct Submission
TITLE	Submitted (14-MAR-1995) Jose R. Botella, Botany Department, University of Queensland, John Hines Building, Brisbane, Queensland

FEATURES	QID 4072,	Australia			
Source	Location/Qualifiers				
	1..1096	/organism="Mangifera indica"			
		/strain="Kensington Royal"			
		/db_xref="taxon:29780"			
		/clone="PMA-1"			
		/tissue_type="fruit"			
		/dev_stage="mature"			
	<1..>1096	/EC_number="4.4.1.14"			
		/function="conversion of ADO-MET to ACC"			
		/note="ACC synthase"			
		/codon_start=1			
		/product="1-aminocyclopropane-carboxylate synthase"			
		/protein_id="AAA84895.1"			
		/db_xref="GI:1143812"			
		/translation="OMGLAENOLCFDLIEDMIKRNPYASICTAGVDEFEKTANEDY HGPERPKAVAKFMVGVRGGRVMPDDRIYMGGVGNANDOIIFCLADGDALVPS YIPAFBDLGMRTGEGELIVPPCDSSFNPDRIOTRALPEAYEKAEANINIKGITNPS NPGLITLDRLTKLSLVFIDEKNIHVCDEITATILPCPEKPVSAVEVQEWDNDIL IHIVYSLSKDMGLPGFVGVIYSYDVAIVNCIRKSSFGLVSSQTUULLASMLSDDEF VEFELEASSKRALKRKHVHIFTFRLEKXGINCLKNGNLFFWMDLRHLLOLFYDAEMKL WGTLINDVKLNVSFGSEHFCEGFRCVCA"			
BASE COUNT	302 a	227 c	255 g	312 t	
ORIGIN					
Query Match	66.1%; Score 15.2;	DB 8;	Length 1096;		
Best Local Similarity	47.8%; Pred. No. 1.4e+03;				
Matches	11; Conservative	7; Mismatches	5; Indels	0; Gaps	0;
QY	1 CANANNCKRASMANCCNRSYTC 23				
	1::: 1:::11				
Db	1088 CAGACTCTGAACCAACGAGCCTC 1066				
RESULT 9					
LOCUS	AF467782/c	1097 bp	mRNA	linear	PLN 18-FEB-2002
DEFINITION	Prunus persica ACC synthase mRNA, partial cds.				
ACCESSION	AF467782				
VERSION	AF467782.1	GI:18699560			
KEYWORDS	.				
SOURCE	Prunus persica.				
ORGANISM	Prunus persica. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.				
REFERENCE	1 (bases 1 to 1097) Yongfeng,J. and Yaozhou,Z. Cloning and expression of the peach ACC synthase gene Unpublished				
AUTHORS	2 (bases 1 to 1097) Yongfeng,J. and Yaozhou,Z.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-JAN-2002) Institute of Biochemistry, Zhejiang University, Kaixuan Road 268, Hangzhou, Zhejiang Province 310029, P. R. China				
RECORD	Location/Qualifiers				
source	1..1097				
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	/db_xref="taxon:3760"				
	<1..>1097				
CDS	/codon_start=1				
	/product="ACC synthase"				
	/protein_id="AAI78631.1"				
	/db_xref="GI:18699561"				
	/translation="QMGLAPNLSFDLIEDMIKRNPKASICTPGEVELKNVALFEODY HGFPERKAVAFMSKARGRYTPDPNNVNGCATGTNELVMCIADPGDAPLVPS HOFTTRDLGWMTGVQIVPVDCDSNNQOITKEALAAVBEAKQKNNISYKLTITNP NFLGKITDRDTLESLEVERISOKNIHLVCDEITYAATVSSPTFCISEYIONTDCPNI IHIVYSLDKMGILPGLRVGISYDVAIVNGRKSSFGLVSSQTUHVLAASMLDDEPMV VARLETSSKRALKRHGVFTGLIEVGINCLRSNAGLCAMDRLRLTLDLPDEEMVL				

BASE COUNT	274 a	265 c	294 g	264 t
ORIGIN	MRVIVNVEFLVPSGSSFRKCEPDMFRCFA"			
Query Match	Best Local Similarity	Score 15.2;	DB 8;	Length 1097;
Matches	11; Conservative	Pred. No. 1.4e+03;	Mismatches 5;	Gaps 0;
QY	1 CANANCCRRAA\$MANCCNRSYTC 23			
Db	1088 CATACCGCGAACCAACCGAGCTTC 1066			
RESULT 10	LOCUS ATU079524/c	1098 bp	mRNA	linear PLN 18-AUG-1998
DEFINITION	Arabidopsis thaliana l-aminocyclopropane-1-carboxylate synthase mRNA, partial cds.			
ACCESSION	U079524			
VERSION	U079524.1			
KEYWORDS	GI:3426257			
SOURCE	Arabidopsis thaliana.			
ORGANISM	Arabidopsis thaliana. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi s (bases 1 to 1098) Valarte,J., Schlagenhaufner,C.D. and Pell,E.U. Induction of an ACC synthase cDNA by ozone in light-grown Arabidopsis thaliana leaves Physiol. Plantum 103, 45-50 (1998)			
REFERENCE	Valarte,J., Schlagenhaufner,C.D. and Pell,E.U. Induction of an ACC synthase cDNA by ozone in light-grown Arabidopsis thaliana leaves Physiol. Plantum 103, 45-50 (1998)			
AUTHORS	Valarte,J., Schlagenhaufner,C.D. and Arteca,R.N.			
TITLE	Direct cloning of a novel ACC synthase gene from Arabidopsis Box 28 (Viikari JI).			
JOURNAL	Submitted 1995-NOV-1996) Plant Biology, University of Helsinki, P.O. Box 28 (Viikari JI), Helsinki 00014, Finland			
FEATURES	location/qualifiers 1..1098 1..organism:"Arabidopsis thaliana" /db_xref="taxon:3702" <1..>1098 /note="ACC synthase; expression is induced by ozone" /codon_start=1 /product="l-aminocyclopropane-1-carboxylate synthase" /protein_id="AAC32251.1" /db_xref="GI:3426258" /translation="OMGPAENOLCGDILRRKWVLKHPKASICTSGVNQSPDIATFOEDYH3LEPEFDROAVAKEMEKTRNNKVRFPDPDPIIVMSGATGAHEVAFCIALAPGGGLVPTTNPPLATLDRKRWGTGVNLVPYVCCHNSNGRIKIYVALDEALAEVAKRSNIKELTLTPNLFMTTSLDRECKLSIVNTNKGIHLINADELYATTPOSEFIISVAETIEITDCNRLLIHVIYSKMGIPGGRVGIVGYVNDRVOYLARKMSFGLVSSOTOLILARKMLSDDEEVDFEIRSKRLRLARRAEITVTGDGIGIGIKAKAGCLFMWDLRLNLTKATFTDSETSETLMRVIVNVEFLVPSGSSFRKCEPDMFRCFA"			
BASE COUNT	295 a	192 c	280 g	331 t
RANGE				
QUERY MATCH	Best Local Similarity	Score 15.2;	DB 8;	Length 1098;
Matches	11; Conservative	Pred. No. 1.4e+03;	Gaps 5;	Indels 0;
QY	1 CANANCCRRAA\$MANCCNRSYTC 23			
Db	1091 CATACTCTGACCAACCCGCGTTTC 1069			
RESULT 11	LOCUS STU070842/c	1098 bp	mRNA	linear PLN 17-JAN-1998
DEFINITION	Solanum tuberosum l-aminocyclopropane-1-carboxylate synthase (STACS5) mRNA, partial cds.			
ACCESSION	U070842			
VERSION	U070842.1			
KEYWORDS	GI:2459544			

SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanaceae; Solanum.
TITLE 1 (bases 1 to 1098)
AUTHORS Schlegenhauer,C.D., Arteca,R.N. and Pell,E.J.
JOURNAL Sequential expression of two 1-aminocyclopropane-1-carboxylate synthase genes in response to biotic and abiotic stresses in potato (Solanum tuberosum L.) leaves
MEDLINE Plant Mol. Biol. 35 (6), 683-688 (1997)
PUBMED 9426590
REFERENCE 2 (bases 1 to 1098)
AUTHORS Schlegenhauer,C.D., Arteca,R.N. and Pell,E.J.
JOURNAL Direct Submission
TITLE Submitted (15-SEP-1996) Horticulture, Penn State University, 103 Tyson Building, University Park, PA 16802 USA
FEATURES
SOURCE 1..1098
CDS
gene /organism="Solanum tuberosum"
/strain="Norland"
/db_xref="taxon:4113"
1..1098
/gene="STACS5"
<1..>1098
/gene="STACS5"
/EC-number="4.4.1.14"
/note="ACC synthase"
/codon_start=1
/product="1-aminocyclopropane-1-carboxylate synthase;
/protein_id="AA86880.1"
/db_xref="GI:2439545"
translation:OMGSLAEQQLCFLLQIEGVYNNPKASCTTGYGVDPDIAIFDYHGLPEFKVAYAKEMEKYGKDVITDPERIVSGATASHESLACDLADPGAFVLPFRNPPEDDLRFETIDLEFPCSSNNPKTKALEIKAQDSNRKLNNRNSMPTDELSRLDLSRGPRGRTIYVNNYDAEALATKAQCSSTISLVMSMDILPVNEFIKSNMKISORDIRDFKIGCGVGICITRKNAAGLFIMDLRFLENSTFNELKLMHIITKVKNLNVSPGCCSFPCSFPSCMRVCFA"

Query Match 66.1% Score 15.2; DB 8; Length 1098;
Best local similarity 47.8%; pred. No. 1.4e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CANANNCKRAAMCANCMRSYTC 23
||| |:::||: ||:::||
Db 1091 CATACTTAACCAACCATGGCTC 1069

RESULT 12
AF239987/c 1100 bp mRNA linear PLN 30-MAR-2000
LOCUS AF239987
DEFINITION Prunus persica ACC synthase ACS1 mRNA, partial cds.
ACCESSION AF239987
VERSION AF239987.1 GI:7341293
KEYWORDS .
SOURCE Prunus persica.
ORGANISM Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE 1 (bases 1 to 1100)
AUTHORS Jin,Y. and Zhang,Y.
JOURNAL Molecular cloning and expression of peach ACC synthase gene
TITLE Unpublished
REFERENCE 2 (bases 1 to 1100)
AUTHORS Jin,Y. and Zhang,Y.
JOURNAL Direct Submission
TITLE Submitted (26-FEB-2000) Institute of Biochemistry, Zhejiang University, Kaixuan Road 268, Hangzhou, Zhejiang 310029, P.R. China

[illegible]

	Db	1091	CACACAGGAAACCACTGGCTC	1069	
RESULT 14					
CPA012577/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
gene					
CDS					
BASE COUNT					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY					
DB					
RESULT 15					
AY120898/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
ORGANISM					

Plate: 0013 row: K column: 07
 Seq primer: CACACAGGAACAGCATGAC
 Class: Plasmid ends
 High quality sequence stop: 103.

FEATURES

source

1..103
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0013K07"
 /clone_1lb="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 41 c 21 g 25 t
 ORIGIN

Query Match 67.0%; Score 15.4; DB 17; Length 103;
 Best Local Similarity 56.5%; Pred. No. 1.4e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 GGNATCCGNGNTTYMGNTNGG 23
 ||:|||||:||||:|
 Db 83 GGACTCCTCGGTTCAGATGGG 61

RESULT 2 128 bp mRNA linear EST 20-DEC-2000
 AM687380
 LOCUS NF009A03RT1F1019 Developing root Medicago truncatula cDNA clone
 DEFINITION NF009A03RT 5', mRNA sequence.
 ACCESSION AM687380
 VERSION AM687380.2 GI:11928221
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 128)
 Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
 Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
 G.D. and Paiva,N.L.
 G.D. and Paiva,N.L.
 Title
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula root library
 Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced g1:7562116.
 Contact: Paiva NL
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7317
 Fax: 580 221 7380
 Email: n.paiva@noble.org

Insert Length: 768 Std Error: 0.00
 Plate: 009 row: A column: 03
 Seq primer: TCACACAGGAACAGCATGAC.
 Location/Qualifiers

FEATURES

source

1..128
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF009A03RT"
 /clone_1lb="Developing root"
 /issue_type="root"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Total RNA was extracted from non-modulated roots of plants grown in 1 mM nitrate medium. Samples were taken at four time points (approximately two days, one, two and six weeks post germination) representing early seedling growth to nitrogen limitation."

BASE COUNT 43 a 22 c 20 g 43 t
 ORIGIN

Query Match 67.0%; Score 15.4; DB 10; Length 128;
 Best Local Similarity 56.5%; Pred. No. 1.5e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 GGNATCCGNGNTTYMGNTNGG 23
 ||:|||||:||||:|
 Db 82 GGATTCCTCGGTTCAGATGG 104

RESULT 3 198 bp DNA linear GSS 17-JUN-2002
 AL751692
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-006E12-014808,
 DEFINITION genomic survey sequence.
 ACCESSION AL751692
 VERSION AL751692.1 GI:21484190
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
 and Weisshaar,B.
 A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 Unpublished
 2
 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 198)
 Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
 Direct Submission
 Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene At3g61510. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpi-zkoeln.mpg.de/GABI-Kat/.

FEATURES

source

1..198
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-006E12-014808"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"									
BASE COUNT	44 a	38 c	48 g	68 t					
ORIGIN									
Query Match	67.0%;		Score 15.4;	DB 17;	Length 198;				
Best Local Similarity	56.5%;		Fred. No. 1.6e-03;						
Matches	13;	Conservative	4;	Mismatches	6;	Indels	0;	Gaps	0;
OY									
1	GGNYTNCNGGTTTGMNFTNGC	23							
Db	11:1111111111111111	77	GGCTCTCCCGGTTTCCGGGTGG	99					
RESULT 4									
LOCUS	233841	332 bp	mRNA	linear	EST 25-MAY-1994				
DEFINITION	ATRS2940 Strasbourg-A Arabidopsis thaliana CDNA clone FA188 5', mRNA sequence.								
ACCESSION	233841								
VERSION	233841.1	GI:493432							
KEYWORDS	EST.								
SOURCE	thale cress.								
ORGANISM	Arabidopsis thaliana								
REFERENCE	Eukaryotic Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.								
AUTHORS	1 (bases 1 to 332)								
TITLE	CNRS								
JOURNAL	The Arabidopsis thaliana transcribed genome: the GDR cDNA program unpublished(1996)								
COMMENT	Contact: Fallipps C., Gigot C.								
FEATURES	Gigot Claude / L512								
Source	Laboratoire de Biologie Molculaire des Plantes - CNRS								
	12 Rue du General Zimmer, 67084 Strasbourg Cedex, France								
	Email: AUBANK@EDC-0-SYRSX.FR.								
	Location/Qualifiers								
	1..332								
	/organism="Arabidopsis thaliana"								
	/strain="ecotype Columbia"								
	/db_xref="taxon:3702"								
	/clone="FA188"								
	/clone_id="Strasbourg-A"								
	/note="Vector: Lambda ZAPII; tissue=sliced leaves of A. thaliana ecotype columbia; clone_library=Strasbourg-A; cloning vector: Lambda ZAPII; Physiological condition: leaves strips incubated 2/3/4 days in liquid culture medium."								
BASE COUNT	86 e	84 c	82 g	78 t	2 others				
ORIGIN									
Query Match	67.0%;		Score 15.4;	DB 14;	Length 332;				
Best Local Similarity	56.5%;		Fred. No. 1.8e-03;						
Matches	13;	Conservative	4;	Mismatches	6;	Indels	0;	Gaps	0;
OY									
1	GGNYTNCNGGTTTGMNFTNGC	23							
Db	11:1111111111111111	281	GGCTCTCCCGGTTTCCGGGTGG	303					
RESULT 5									
LOCUS	AU092777	351 bp	mRNA	linear	EST 03-APR-2002				
DEFINITION	AU092777 rice gallus Oryza sativa (japonica cultivar-group) CDNA clone C53337, mRNA sequence.								
ACCESSION	AU092777								

```


|                       |                                                                                                                                                                                                                                                                                                       |                                    |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------|
| VERSION               | AU092777.1                                                                                                                                                                                                                                                                                            | GI:8527962                         |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                  |                                    |
| SOURCE                | Oryza sativa (japonica cultivar-group).                                                                                                                                                                                                                                                               |                                    |
| ORGANISM              | Oryza sativa (japonica cultivar-group)                                                                                                                                                                                                                                                                |                                    |
|                       | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;                                                                                                                                                                                                                                    |                                    |
|                       | Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;                                                                                                                                                                                                                                           |                                    |
|                       | Eharistolidae; Oryzaceae; Oryza.                                                                                                                                                                                                                                                                      |                                    |
| REFERENCE             | 1 (bases 1 to 351)                                                                                                                                                                                                                                                                                    |                                    |
| AUTHORS               | Sasaki,T. and Yamamoto,K.                                                                                                                                                                                                                                                                             |                                    |
| TITLE                 | Rice cDNA from callus (2000)                                                                                                                                                                                                                                                                          |                                    |
| JOURNAL               | Unpublished (2000)                                                                                                                                                                                                                                                                                    |                                    |
| COMMENT               | Contact: Takuji Sasaki<br>National Institute of Agrobiological Resources<br>Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki<br>305-8602, Japan<br>Tel.: 81-298-38-7441<br>Fax: 81-298-38-7468<br>Email: tessakai@abr.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/<br>PROJECT = "RGPR" |                                    |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                   |                                    |
| SOURCE                | 1..351                                                                                                                                                                                                                                                                                                |                                    |
|                       | /organism="Oryza sativa (japonica cultivar-group)"                                                                                                                                                                                                                                                    |                                    |
|                       | /cultivar="Nipponbare"                                                                                                                                                                                                                                                                                |                                    |
|                       | /db_xref=taxon:39947"                                                                                                                                                                                                                                                                                 |                                    |
|                       | /clone="C53537"                                                                                                                                                                                                                                                                                       |                                    |
|                       | /cnote_jlb="Rice callus"                                                                                                                                                                                                                                                                              |                                    |
|                       | /ncote=vector: pbnucript II SK+ site_1: SalI; Site_2:                                                                                                                                                                                                                                                 |                                    |
|                       | NotI; CDNA prepared from rice callus mRNAs by using                                                                                                                                                                                                                                                   |                                    |
|                       | o15io(qt) as a primer and ligating to the SalI-NotI site                                                                                                                                                                                                                                              |                                    |
|                       | of PBNUscript II SK+ phagemid."                                                                                                                                                                                                                                                                       |                                    |
| BASE COUNT            | 63 a 128 c 101 g 57 t -                                                                                                                                                                                                                                                                               | others 2 others                    |
| ORIGIN                | -                                                                                                                                                                                                                                                                                                     |                                    |
| Query Match           | 67.0% Score 15.4 DB 9 Length 351;                                                                                                                                                                                                                                                                     |                                    |
| Best Local Similarity | 56.5%; Pred No 1.g.e+03;                                                                                                                                                                                                                                                                              |                                    |
| Matches               | 13 Conservative                                                                                                                                                                                                                                                                                       | 4 Mismatches 6 Indels 0 Gaps 0;    |
| OY                    | 1 GCNTNCNGCNTTGMGRTNG 23                                                                                                                                                                                                                                                                              |                                    |
| Dn                    | 11...1111111111111111                                                                                                                                                                                                                                                                                 |                                    |
|                       | GACCTCCCGGCCTTCGGCTCG 320                                                                                                                                                                                                                                                                             |                                    |
| RESULT 6              |                                                                                                                                                                                                                                                                                                       |                                    |
| LOCUS                 | AVA10488                                                                                                                                                                                                                                                                                              | 428 bp mRNA linear EST 23-MAY-2000 |
| DEFINITION            | AVA10488 Lotus japonicus young plants (two-week old) lotus                                                                                                                                                                                                                                            |                                    |
|                       | japonicus cDNA clone MWL0Jse12_r 5'', mRNA sequence.                                                                                                                                                                                                                                                  |                                    |
| ACCSSION              | AVA10488                                                                                                                                                                                                                                                                                              |                                    |
| VERSION               | AVA10488.1 GI:7723342                                                                                                                                                                                                                                                                                 |                                    |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                  |                                    |
| SOURCE                | Lotus japonicus.                                                                                                                                                                                                                                                                                      |                                    |
| ORGANISM              | Lotus japonicus                                                                                                                                                                                                                                                                                       |                                    |
|                       | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;                                                                                                                                                                                                                                    |                                    |
|                       | Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;                                                                                                                                                                                                                                         |                                    |
|                       | Rosidae; eurosids I; Fabiales; Fabaceae; Papilionideae; Lotaeae;                                                                                                                                                                                                                                      |                                    |
|                       | lotus.                                                                                                                                                                                                                                                                                                |                                    |
|                       | 1 (bases 1 to 428)                                                                                                                                                                                                                                                                                    |                                    |
| REFERENCE             | Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.                                                                                                                                                                                                                                                        |                                    |
| AUTHORS               | Generation of 7137 non-redundant expressed sequence tags from a                                                                                                                                                                                                                                       |                                    |
| TITLE                 | legume, Lotus japonicus                                                                                                                                                                                                                                                                               |                                    |
| JOURNAL               | DNA Res. 7 (2), 127-130 (2000)                                                                                                                                                                                                                                                                        |                                    |
| MEDLINE               | 20277479                                                                                                                                                                                                                                                                                              |                                    |
| COMMENT               | Contact: Yasukazu Nakamura<br>The First Laboratory for Plant Gene Research<br>Kazusa DNA Research Institute<br>Yana 1532-3 Kisarazu Chiba 292-0812, Japan<br>Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.<br>location/Qualifiers                                               |                                    |
| FEATURES              | 1..428                                                                                                                                                                                                                                                                                                |                                    |
| SOURCE                | /organism="Lotus japonicus"                                                                                                                                                                                                                                                                           |                                    |
|                       | /db_xref=taxon:34303"                                                                                                                                                                                                                                                                                 |                                    |
|                       | /clone="MWL0Jse12_r"                                                                                                                                                                                                                                                                                  |                                    |
|                       | /cnote_jlb="Lotus japonicus young plants (two-week old)"                                                                                                                                                                                                                                              |                                    |


```

/dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; Isolate=Myakojima MG-20"

BASE COUNT

133 a 116 c 80 g 99 t

Query Match

Best Local Similarity 56.5%; Pred. No. 1.9e+03;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGGNTTGMRTNGC 23

DB 374 GGTTCCCGATTCAGATTGG 396

RESULT 7
 BFL12525 431 bp mRNA linear EST 18-MAY-2001

DEFINITION EST140115 tomato breaker fruit Lycopersicon esculentum cDNA clone

ACCESSION BFL12525
 CLE641J5 5' sequence, mRNA sequence.

VERSION BFL12525.1 GI:10942215

KEYWORDS EST

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 431)

Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,

Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,

Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley

,S.D.

Generation of ESTs from tomato fruit tissue, breaker stage

Unpublished (2000)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1..431

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CLE641J5"

/clone_lib="tomato breaker fruit"

/tissue_type="pericarp"

/dev_stage="breaker"

/lab_host="SOLR"

/note="Vector: pBluescriptSKmCunadapt; Site_1: EcoRI;

Site_2: XhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research. Fruit

were harvested at the breaker stage (first sign of

lycopene accumulation on the blossom end of fruit). Fruit

were cut in half and the seeds and locules were discarded

prior to freezing the pericarp."

BASE COUNT 132 a 76 c 82 g 141 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 12; Length 431;

Best Local Similarity 56.5%; Pred. No. 1.9e+03;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGGNTTGMRTNGC 23

DB 232 GGTTCCCGATTCAGATTGG 254

RESULT 8

AI898708 450 bp mRNA linear EST 18-MAY-2001

LOCUS

AI898708

DEFINITION

EST14287 tomato developing/immature green fruit Lycopersicon

esculentum cDNA clone CLEM5013, mRNA sequence.

ACCESSION BE458995

VERSION BE458995.1 GI:9503297

KEYWORDS EST

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 459)

Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,

Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,

Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley

,S.D.

Generation of ESTs from tomato fruit tissue, immature green

Unpublished (2000)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1..450

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CLE63K4"

/clone_lib="tomato ovary, TAMU"

/tissue_type="carpel"

/dev_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab_host="XLI-Blue WRF"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; cLED - Tomato Carpel EST library. OligoDT-primed and

directionally cloned cDNA in vector Lambda Zap II with 5'

and 3' ends located at the EcoRI and XhoI sites,

respectively."

BASE COUNT 146 a 81 c 84 g 139 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 9; Length 450;

Best Local Similarity 56.5%; Pred. No. 2e+03;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGGNTTGMRTNGC 23

DB 421 GGATTTCCAGATTTCAGATTGG 443

RESULT 9

BE458995

DEFINITION

EST14287 tomato developing/immature green fruit Lycopersicon

esculentum cDNA clone CLEM5013, mRNA sequence.

ACCESSION BE458995

VERSION BE458995.1 GI:9503297

KEYWORDS EST

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 459)

Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,

Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,

Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley

,S.D.

Generation of ESTs from tomato fruit tissue, immature green

Unpublished (2000)

Contact: CUGI

Clemson University Genomics Institute

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA.
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES

source

1. 459
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="CLEM5013"
/tissue_type="tomato developing/immature green fruit"
/tissue_type="fruit"
/dev_stage="immature green (5-35 days post-anthesis)"
/lab_host="SOLR"
/note="Vector: pBluescriptSKmCquadap; Site_1: EcoRI;
Site_2: XhoI; Fruit were tagged at 5 dpa (0.5 cm) and
harvested at 7 day intervals through 35 dpa. Equal masses
of tissue from each stage were combined (including seeds
and locules) prior to mRNA isolation."

BASE COUNT
ORIGIN

165 a 80 c 79 g 135 t

Query Match 67.0%; Score 15.4; DB 10; Length 459;
Best Local Similarity 56.5%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCGTTCGTTAGCGTTGG 23

Db 320 GGGTTCTCGATTAGCGTTGG 342

RESULT 10
LOCUS

N65643 479 bp mRNA linear EST 05-JAN-1998
DEFINITION 20683 Lambda-PRL2 Arabidopsis thaliana cDNA clone 2401277, mRNA
Sequence.

ACCESSION N65643
VERSION N65643.1 GI:1217269

KEYWORDS EST.
SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Ericales; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 479)
Neman, J., deBuit, F.J., Green, P., Keegstra, K., Kende, H., McIntosh,
J., Orlowski, J., Raikhet, N., Somerville, S., Thomasow, M., Reisel,
E., and Somerville, C.

FEATURES
AUTHORS

TITLE Gene clone: a summary of methods for accessing results from
large scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL Plant Physiol. 106, 1241-1255 (1994)

COMMENT 5148729
Contact: Thomas Newman
MSU/DOE Plant Research Laboratory
Michigan State University
MSU/DOE Plant Research Laboratory
Michigan State University, Plant Biology Bldg., E.
Lansing, MI 48824
Tel: 517-383-9168
Fax: 517-383-9168
Email: 2:333@clm.clemson.edu
Seq primer 47 dpa clones

FEATURES
source

1. 479
/organism="Arabidopsis thaliana"
/strain="var. columbia"
/db_xref="taxon:3702"
/clone_lib="lambda-PRL2"
/note="Vector: lambda Zip-lox; Site_1: SalI; Site_2: NotI;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings, 2) tissue culture

grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-lox. The cDNA
inserts were directionally cloned with SalI-NotI arms using
0190 dt primed cDNA.

BASE COUNT 106 a 97 c 121 g 136 t 19 others

Query Match 67.0%; Score 15.4; DB 14; Length 479;
Best Local Similarity 56.5%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCGTTCGTTAGCGTTGG 202

Db 180 GGGTTCTCGATTAGCGTTGG 342

RESULT 11 487 bp DNA linear GSS 25-APR-2002
LOCUS BH803717
DEFINITION 1008103H01.x1 1008 - Rescuedu Grid I Zea mays genomic, DNA
Sequence.

ACCESSION BH803717
VERSION BH803717.1 GI:20319176

KEYWORDS GSS.
SOURCE Zea mays.

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 487)
Walbot, V.

AUTHORS Maize genomic sequences found using engineered Rescuedu transposon
unpublished (2001)

TITLE Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

COMMENT Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008103 row: 5
Class: transposon-tagged.

FEATURES
source

1. 487
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - Rescuedu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuedu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
Rescuedu is a 4.9 kb, modified maize transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuedu, go to the web
site www.zmdb.iastate.edu and follow the links for
Rescuedu. Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin.

BASE COUNT 69 a 165 c 172 g 81 t

Query Match 67.0%; Score 15.4; DB 17; Length 487;
Best Local Similarity 56.5%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTCNCNGNTTYMGNTNGS 23
 Db 452 GGCTTCCTCCGGGTTCCGGCGTGG 474

RESULT 12
 LOCUS A1993687 496 bp mRNA linear EST 08-SEP-1999
 DEFINITION 701497137 A. thaliana, Ohio State clone set Arabidopsis thaliana
 CDNA clone 701497137, mRNA sequence.

ACCESSION A1993687
 VERSION A1993687.1 GI:5840592
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 496)
 Chen, J., Momiya, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
 Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,
 Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,
 Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
 Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murty, L.,
 Turner, C., Krikorian, S., Elder, L. and Hanson, D.
 Arabidopsis thaliana Gene Expression Microarray
 Unpublished (1999)
 CONTACT: David Smoller, Ph.D.
 Genome Systems, Inc., a wholly owned subsidiary of Incyte
 Pharmaceuticals, Inc.
 4633 World Parkway Circle, St. Louis, MO 63134, USA
 Tel: 877-577-2733
 Fax: 314-427-3324
 Email: service@genomesystems.com.
 Location/Qualifiers
 1..496
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="701497137"
 /note="CDNA library was made from selected clones from the
 Arabidopsis thaliana Ohio State clone set."

BASE COUNT 134 a 102 c 131 g 129 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 9; Length 496;
 Best Local Similarity 56.5%; Pred. NO. 2e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTCNCNGNTTYMGNTNGS 23
 Db 179 GGCTTCCTCCGGGTTCCGGCGTGG 201

RESULT 13
 LOCUS AA650853 505 bp mRNA linear EST 31-OCT-1997
 DEFINITION 30967 Lambda-PRL2 Arabidopsis thaliana CDNA clone 288D277, mRNA
 sequence.

ACCESSION AA650853
 VERSION AA650853.1 GI:2580945
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 505)
 Newman, T., deBruin, F. J., Green, P., Keegstra, K., Kende, H., McIntosh,
 L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomasnow, M., Retzel,
 E. and Somerville, C.
 Genes galore: a summary of methods for accessing results from

JOURNAL
 MEDLINE
 COMMENT
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Plant Physiol. 106, 1241-1255 (1994)
 95148729
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313cne@lhm.cl.msu.edu
 Seq primer: 77 dye primer.
 Location/Qualifiers
 1..505
 /organism="Arabidopsis thaliana"
 /strain="var columbia"
 /db_xref="taxon:3702"
 /clone="288D277"
 /note="Vector: lambda Zip-lox; Site-1: Sal; Site-2: Not;
 Lambda PRL2 is a cDNA library derived from equal
 quantities of 4 pools of mRNA. The mRNA sources were 1) 7
 day germinated etiolated seedlings; 2) tissue culture
 grown roots; 3) staged plants half with 24 hour light
 cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
 same plants as 3 but aerial tissue (stems, flowers and
 siliques). The vector is BRL's lambda Zip-lox. The cDNA
 inserts were directionally cloned with Sal-Not arms using
 oligo dt primed cDNA."

BASE COUNT 128 a 107 c 127 g 124 t 19 others

ORIGIN

Query Match 67.0%; Score 15.4; DB 9; Length 505;
 Best Local Similarity 56.5%; Pred. NO. 2e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTCNCNGNTTYMGNTNGS 23
 Db 178 GGCTTCCTCCGGGTTCCGGCGTGG 200

RESULT 14
 LOCUS BF276958 519 bp mRNA linear EST 07-MAR-2001
 DEFINITION GA_Eb0026C04f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum CDNA clone GA_Eb0026C04f, mRNA sequence.

ACCESSION BF276958
 VERSION BF276958.1 GI:11208028
 KEYWORDS EST.
 SOURCE Gossypium arboreum.
 ORGANISM Gossypium arboreum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 1 (bases 1 to 519)
 Wing, R. A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry,
 D., Wood, T. C., Leslie, A. and Wilkins, T. A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 Unpublished (2000)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: 7AATACGACATCATATAGG
 High quality sequence stop: 514.
 Location/Qualifiers
 1..519
 /organism="Gossypium arboreum"
 /strain="AKA"

FEATURES
 source

Search completed: March 10, 2003, 06:42:37
 Job time : 1343 secs

BASE COUNT 154 a 83 c 113 g 169 t
 ORIGIN

Query Match 67.0%; Score 15.4; DB 12; Length 519;

Best Local Similarity 56.5%; Pred No. 26+03; 6; Indels 0; Gaps 0;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGCNTVMGNRTNG 23

DB 133 GGCTCCCTCGCTTTTACAGTTGG 155

RESULT 15
 A1898837 521 bp mRNA linear EST 18-MAY-2001
 LOCUS EST268280 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
 DEFINITION CLE035F22 mRNA sequence.
 ACCESSION A1898837
 VERSION A1898837.1 GI:5604739
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.

REFERENCE 1 (bases 1 to 521)
 Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
 Liang,J., Upton,J., Romning,C.M., Craven,M.B., Fujii,C.Y., Bowman,
 C.D., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,
 S.D. and Giovannoni,J.
 Generation of ESTs from tomato carpel tissue

TITLE Unpublished (1999)
 JOURNAL Contact: CBGI
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES
 source 5 prime sequence.
 Location/Qualifiers
 1..521

Location/Qualifiers
 1..521
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLE035F22"
 /clone_lib="tomato ovary, TAMU"
 /tissue_type="carpel"
 /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
 /lab_host="XLI-Blue MRF"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; CLE03 - tomato carpel EST library. OligodT-primed and
 directionally cloned cDNA in vector lambda Zap II with 5'
 and 3' ends located at the EcoRI and XhoI sites,
 respectively. 98 g 155 t

BASE COUNT 175 a 93 c 98 g 155 t
 ORIGIN

Query Match 67.0%; Score 15.4; DB 9; Length 521;

Best Local Similarity 56.5%; Pred No. 26+03; 6; Indels 0; Gaps 0;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGCNTVMGNRTNG 23

DB 399 GGATTCAGATTCAGATTGG 421


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Run on:      March 10, 2003, 05:12:24 ; Search time 1330 Seconds
              (without alignments)
              280.072 Million cell updates/sec
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Title:	US-09-975-842-3
Perfect score:	23
Sequence:	1 cananckraasmancnrslc 23

Scoring table: IDENTITY_NUC
Gap03 10.0 : Gapext 1.0

Searched: 16151066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

Database :

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1:  «m_estba:*
2:  «m_estbm:*
3:  «m_estin:*
4:  «m_estnu:*
5:  «m_estov:*
6:  «m_estpl:*
7:  «m_estov:*
8:  «m_htc:*
9:  «b_est2:*
10: «b_est1:*
11:  «b_htc:*
12:  «b_est3:*
13:  «b_est4:*
14:  «b_est5:*
15:  «m_estun:*
16:  «m_estom:*
17:  «d_gstb:*
18:  «d_gstc:*
19:  «d_gstn:*
20:  «d_gstp:*
21:  «d_gstv:*
22:  «m_gstn:*
23:  «m_gstm:*
24:  «m_gstms:*
25:  «m_gstms_piv:*
26:  «m_gstms_rtd:*
27:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.2	66.1	231	1	BA44016	BA44016
2	15.2	66.1	1	10	BB59577	BB59577
3	15.2	66.1	10	10	BB40123	BB40123
4	15.2	66.1	342	10	BB40126	BB40126
5	15.2	66.1	351	14	BM14937	BM14937
6	15.2	66.1	360	17	AA02070	AA02070

[illegible]

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
AV440166	221 bp	Arabidopsis thaliana above-ground two to six-week old Arabidopsis thaliana cDNA clone AP045d02_1 3', mRNA sequence.

VERSION AV440166.1 GI:7610522

SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE

JOURNAL
MEDLINE

COMMENT:

FEATURES

0
0
5
1
0

100

```

/db_xref="taxon:3702"
/clone="APD45602.f"
/clone_lib="Arabidopsis thaliana above-ground organ two to
six-week old"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT      71 a      49 c      33 g      68 t

ORIGIN
Query Match          66.1%; Score 15.2; DB 10; Length 221;
Best Local Similarity 47.8%; Pred. NO.1.ee+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANNCRAASMANCNRSTYC 23
||| : ||::|| ::||
Db      114 CAGATTCGAAACCATCGTTC 136

RESULT 2
BB595771/c        270 bp    mRNA    linear    EST 30-NOV-2000
LOCUS            BB595771 RIKEN full-length enriched, 16 days embryo head Mus
DEFINITION       BB595771 RIKEN clone Cl30005F08 5', mRNA sequence.
ACCESSION        BB595771
VERSION          BB595771.1 GI:11492373
KEYWORDS         EST.
SOURCE           house mouse.
ORGANISM         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
1 (bases 1 to 270)
Alizawa,K., Akahita,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P.,
Hanaagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodojama,Y.,
Imotani,K., Ishii,Y., Itoh,M., Itawa,M., Kawai,J., Kojima,Y., Konno,
H., Kusabebe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,T., Shingawa,A.,
Shiraki,T., Sogabe,T., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,
T., Toya,T., Watabiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Alizawa,K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscl.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S., Sasakihara,Y.,
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermosensitization and thermocoregulation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Katsunuma,T., Akiyama,U., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y.,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
Location/Qualifiers
1..270
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

```

	/clone="I30005F08"
	/clone_lib="RIKEN full-length enriched, 16 days embryo
	head"
	/sex="mixed"
	/tissue_type="head"
	/dev_stage="16 days embryo"
	/lab_host="DH10B"
	/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
	GAGGAGAAGAAAGATCCAGAGCTTTTTTTTTTTTTTTNN 3'] . cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
	GAGGAGAAGATTTCGAGTTAATTAATTAATTCACCCCCCCCCC 3'] . cDNA was cloned into the XhoI and BamHl sites. Vector: a modified pluscript KS(+) after bulk excision from Lambda
	FHC I "
BASE COUNT	55 a 56 c 102 g 57 t
ORIGIN	
Query Match	66.1%; Score 15.2; DB 10; Length 270;
Best Local Similarity	47.8%; Pred. No. 1.8e+03;
Matches	11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
OY	1 CANNANCKRAASMANCCNRSTYC 23
Db	219 CACACGCTGAACCACCCAGGTTC 197
RESULT 3	
LOCUS	BE401232/c 300 bp MRNA linear EST 21-JUL-2000
DEFINITION	CNM01PLD232 ITFC CNM wheat Powdery Mildew Resistant Library
ACCESSION	ITflicum aestivum cDNA clone CNM01PLD232, mRNA sequence.
VERSION	BE401232
KEYWORDS	BE401232.1 GI:9360700
SOURCE	EST.
ORGANISM	wheat. bread wheat. Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum. 1 (bases 1 to 300)
REFERENCE	Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier, S., Dubcovsky,J., Feuillat,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Quniset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrellis,M., Warburton,M. and Wenzel,G. International Triticaceae ESP Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae Undpublished (2000) Contact: Jia J Key Lab. of Crop Germplasm & Biotechnology Inst. of Crop Germplasm Resources Beijing 100081 PR CHINA Tel: 86 1 62186623 Fax: 86 1 62186629 Email: jizengemini.cnc.ac.cn international_triticaceae_EST_Cooperative_(ITEC) http://wheat.pw.usda.gov/genome .
TITLE	
JOURNAL	
COMMENT	Location/Qualifiers 1..300 /organism="Triticum aestivum" /cultivar="Powdery Mildew Resistant line" /db_xref="taxon:4565" /clone="CNM01PLD232"
FEATURES	
source	

```

Query Match      66.1%; Score 15.2; DB 10; Length 300;
Best Local Similarity 52.2%; Pvec No.19e+03;
Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

OY      1 CANANCKRASMANCNSNYTC 23
        |||:::|||::|||
Db       125 CAGACCGGACACCANCCGGGCTC 103

RESULT 4
BM149376/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 342)
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R., Jr.,
Gunaratna,P.H., Muzny,D., Bonck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric leukemia CDNA Sequencing Project (2001)
Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: c.genes@txccc.org
Seq primer: M13 primer.
Location/Qualifiers
1..342
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="TCAP1199"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HSC project-TCAA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
/note=Vector: lambda PSB: Site.1: BamHI; Site.2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GAGACATCGAGCGGCAGAGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then de tailed. Second strand
was primed with "BamH-dc primer
[5'AGAGACTCGATCGCGGCCGCAATATATATAT(C) 3']".
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda psb vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carlnici P, Westover A, Nishiyama Y, Ohsumi T,
Ichih M, Nagaoaka S, Sasakino, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, June 28, 1997")
DNA Res 4: 1, 61-6, June 28, 1997")
BASE COUNT
51 a 100 c 97 t

```

[illegible]

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3242 row: M column: 8
 Class: BAC ends
 High quality sequence stop: 360.

FEATURES
 Source
 1..360
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="plate=3242 Col=8 Row=M"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT
 69 a 132 c 45 g 112 t 2 others

ORIGIN
 Query Match 66.1%; Score 15.2; DB 17; Length 360;
 Best Local Similarity 47.8%; Pred. No. 2e+03;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRAASMANCCRSYTC 23
 ||| 1::||:1 11:::11
 Db 302 CATAGTCGACACATCCTACCTC 324

RESULT 7
LOCUS A1608175/c 361 bp mRNA linear EST 21-APR-1999
DEFINITION vc83h10.y1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone
 IMAGE:789667 5' similar to TR:063418 Q63418 PROTOCADHERIN 3. ;
 mRNA sequence.
ACCESSION A1608175
VERSION A1608175.1 GI:4617342
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 361)
 Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Waller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 The Washu-NCI Mouse EST Project 1999
 Unpublished (1999)
COMMENT Contact: Marra M/Washu-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:474075
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Possible reversed clone: similarity on wrong strand
 Seq primer: Primer name ambiguous
 High quality sequence stop: 161.
 Location/Qualifiers

FEATURES
 Source

source
 1..361
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:789667"
 /clone_lib="Ko mouse embryo 11 5dpc"
 /sex="pooled"
 /tissue="embryo"
 /dev_stage="11.5dpc"
 /lab_host="DH10B"
 /note="Organ: embryo; Vector: pSPOR1; Site_1: SalI; Site_2: NotI; Total RNAs were extracted from 11.5 dpc embryos (excluding placenta and yolk sac). The double-stranded cDNA was synthesized with an oligo (dT)-1 primer GAGAGGACTAGTTCAGATCGGACGCCGCTTTT TTTT TTTT 3'. The cDNAs were ligated to LL-Sal3A: 5' GCTATTGACCTCGACTATCC 3' and LL-Sal3B: 5' GATAGTCGACGTCAT 3'. The cDNAs were size-selected and amplified by long-range PCR using Ex Taq polymerase for 18 cycles. The PCR-amplifiable cDNA mixture went through one round of equalization and was digested with SalI/NotI and cloned into the SalI/NotI sites of the pSPOR1 plasmid vector (Life Technologies). The library was constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong Wang."

BASE COUNT
 69 a 107 c 105 g 78 t 2 others

ORIGIN
 Query Match 66.1%; Score 15.2; DB 9; Length 361;
 Best Local Similarity 47.8%; Pred. No. 2e+03;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRAASMANCCRSYTC 23
 ||| 1::||:1 11:::11
 Db 168 CACACACTGAACACCCGGCCTC 146

RESULT 8
LOCUS BE353050/c 406 bp mRNA linear EST 19-JUL-2000
DEFINITION Dg1_3.F05.g1_A002 Dark Grown 1 (Dg1) sorghum bicolor cDNA, mRNA
 sequence.
ACCESSION BE353050
VERSION BE353050.1 GI:9281026
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 406)
 Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
 ,L.H.
 An EST database from Sorghum: dark-grown seedlings
 Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@pratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: 77
 High quality sequence start: 36
 High quality sequence stop: 406
 POLYA=Yes.
 Location/Qualifiers

FEATURES
 Source
 1..406
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"

```

/clone.lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
lambda zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced by mass excision."
BASE COUNT      105 a      88 c      117 g      96 t
ORIGIN
Query Match      66.1%; Score 15.2; DB 10; Length 406;
Best Local Similarity 47.8%; Pred. No. 2.1e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 CANANCKR2ASMANCNRSTC 23
Db      135 CACACCGCTGACCGCGGCTC 113

RESULT 9
LOCUS      BE209956/c      410 bp      mRNA      linear      EST 04-DEC-2001
DEFINITION      so37b07.y1 Gm-cl039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl035-110 5' similar to TR:043201 Q43201
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.
ACCESSION      BE209956
VERSION        BE209956.1 GI:8825235
KEYWORDS
SOURCE        soybean.
ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE      1 (bases 1 to 410)
AUTHORS      Shoemaker,R., Keim,P., Vodkin,L., Expelling,J., Coryell,V., Khanna
A., Bolla,B., Marita,M., Hillier,L., Kucaba,T., Martin,D., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
Y., Persop,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
R., Ralter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
R., Matanson,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: culetresgen.com
Insert Length: 1204 Std Error: 0.00
High qual. seq. stop: 409.
Location/Qualifiers
1..410
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-110"
/clone.lib="Gm-cl039"
/tissue.type="whole seedling without cotyledons"
/lab.host="DH10B"
/note="vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This

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library was constructed by Dr. Randy Shoemaker."
BASE COUNT      97 a      72 c      110 g      130 t      1 others
ORIGIN
Query Match      66.1%; Score 15.2; DB 10; Length 410;
Best Local Similarity 47.8%; Pred. No. 2.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 CANANCKR2ASMANCNRSTC 23
Db      323 CAAGAAGCAACCATCCAGGCTC 301

RESULT 10
LOCUS      AL502553      413 bp      mRNA      linear      EST 04-JAN-2001
DEFINITION      AL502553 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone
HM07P07u 3', mRNA sequence.
ACCESSION      AL502553
VERSION        AL502553
KEYWORDS
SOURCE        EST.
ORGANISM      Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 413)
AUTHORS      Michalek,W., Meschke,M., Pleissner,K.-P. and Graner,A.
TITLE          EST sequencing and analysis in barley
JOURNAL        Unpublished (2000)
COMMENT        Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: M13mt primer for 3' end.
Location/Qualifiers
1..413
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HM07P07u"
/clone.lib="Hordeum vulgare Barke roots"
/tissue.type="roots"
/lab.host="XL01R"
/note="vector: Plasmid pBK-CMV; Site_1: EcoRI; Site_2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: EcoRI (3'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the K1L, in most
cases the EcoRI site is NOT present, as well as the EcoRI
adapter. Average insert size is 1 kb. Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'- and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp."
BASE COUNT      84 a      116 c      92 g      121 t
ORIGIN
Query Match      66.1%; Score 15.2; DB 9; Length 413;
Best Local Similarity 47.8%; Pred. No. 2.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 CANANCKR2ASMANCNRSTC 23
Db      256 CACACCGCTGACCGCGGCTC 278

RESULT 11
LOCUS      AV820681      420 bp      mRNA      linear      EST 01-APR-2002
DEFINITION      AV820681 RAP111 Arabidopsis thaliana cDNA clone RAP111-11-L09 3',
mRNA sequence.
ACCESSION      AV820681

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VERSION	AV820681.1	GI:19862660	EST.	thale cress.	Arabidopsis thaliana	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; Brassicales; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsi
ORGANISM	Arabidopsis thaliana					
REFERENCE	1 (bases 1 to 420)					
AUTHORS	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.					
TITLE	Large scale analysis of Arabidopsis full-length cDNA (2002b)					
JOURNAL	Unpublished (2002)					
COMMENT	Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: msek@rtc.riken.go.jp Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda ETC-1 vector (Carninci et al., submitted for publication), digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.					
FEATURES	Location/Qualifiers					
SOURCE	1..420					
	/organism="Arabidopsis thaliana"					
	/db_xref="taxon:3702"					
	/clone="RAF11-11-L09"					
	/clone_id="RAF11"					
	/dev_stage="plants at various developmental stages from germination to mature seeds"					
	/lab_host="DH10B"					
	/note="Site_1: BamHI; Site_2: SalI; subjected to various treatments (dehydration, cold, high salt, ABA, heat and UV). Dark-grown plants"					
BASE COUNT	122 a 105 c 64 g 129 t					
ORIGIN						
Query Match	66.1%; Score 15.2; DB 10; Length 420;					
Best Local Similarity	47.8%; Pred. NO. 2.2e+03;					
Matches	11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;					
QY	1 CANANNCKRAASMANCNRSYTC 23					
	::: :::					
Db	170 CAGATCGGACCACTCGTGTC 192					
RESULT 12						
LOCUS	AV808550 423 bp mRNA linear EST 29-MAR-2002					
DEFINITION	AV808550 RAF19 Arabidopsis thaliana cDNA clone RAF109-55-El5 3', mRNA sequence.					
ACCESSION	AV808550					
VERSION	AV808550.1					
KEYWORDS	GI:19842535					
SOURCE	EST.					
ORGANISM	thale cress.					
	Arabidopsis thaliana					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.					
REFERENCE	1 (bases 1 to 423)					
AUTHORS	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.					
TITLE	Large scale analysis of Arabidopsis full-length cDNA (2002b)					
JOURNAL	Unpublished (2002)					
COMMENT	Contact: Motoaki Seki					

	Pfizer Functional Genomics Research Group Riken Genetic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: mseki@rct.taken.go.jp
	An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda Phage vector (Carlini et al.), submitted for publication) digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web site (http://www.gsc.taken.go.jp/e/plant/index_e.html) for further details.
FEATURES	Location/Qualifiers
source	1..423 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /cclone="RAFL09-55-E15" /cclone_lib="RAF19" /dev_stage="plants at various developmental stages from germination to mature seeds" /lab_host="DH10B" /note="Site-1: BamHI; Site-2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT	121 a 101 c 72 g 129 t
ORIGIN	
Query Match	66.1%; Score 15.2; DB 10; Length 423;
Best Local Similarity	47.8%; Pred. No. 2.e+03;
Matches	11: Conservative 7: Mismatches 5; Indels 0; Gaps 0;
OY	1 CANANCKRAMCNCNRSTYC 23 : :: : : :: :
Dn	114 CAGATACGGAACCATCTGTTC 136
RESULT 13	
AZ863097	431 bp DNA linear GSS 21-FEB-2001
LOCUS	ZM0171003F Mouse 10kb plasmid ucncim Library Mus musculus genomic
DEFINITION	c1one U00G2M0171003 F, DNA sequence.
ACCESSION	AZ863097
VERSION	AZ863097.1 GI:13061059
KEYWORDS	GSS.
SOURCE	house mouse. Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	I (bases 1 to 431) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rogace,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weiss,R.
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts Unpublished (2000)
TITLE	Contact: Robert B. Weiss University of Utah Genome Center University of Utah
JOURNAL	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177
COMMENT	Email: ddunng@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0171 row: O column: 03 Seq primer: CGTGTAAACGACGCCAAGT Class: plasmid ends High quality sequence stop: 431. Location/Qualifiers 1..431 /organism="Mus musculus"
FEATURES	
source	

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U082M0171003"
/clone_lib="Mouse 10kb plasmid U082M0171003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a C.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
87 a 143 c 112 g 89 t

Query Match 66.1% Score 15.2: DB 17: Length 431:
Best Local Similarity 47.8%: Pred No. 2.2e+03:
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRA5MANCCRSYTC 23
Db 372 CAGATGCTGAGAGACCCGCCCTC 394

RESULT 14
LOCUS B0468428/c 455 bp mRNA linear EST 30-MAY-2002
DEFINITION HM01D16T HM Hordeum vulgare cDNA clone HM01D16 5-PRIME, mRNA
sequence.
B0468428
B0468428.1 GI:21276210
EST.
SOURCE
ORGANISM
Hordeum vulgare.
Hordeum vulgare.
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
1 (bases 1 to 455)
Zhang, H., Meschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein, Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3 06466, Gatersleben, Germany
Tel: 039483-5522
Fax: 039483-5595
Email: stein@ipk-gatersleben.de
Insert Length: 455 Std Error: 0.00
Plate: 1 row: D column: 16
Seq primer: T3.
Location/Qualifiers
1..455
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HM01D16"
/clone_lib="HM"
/tissue_type="male inflorescences"
/gen_stage="male inflorescences (approx. 2 mm in size),

```

```

green anther stage"
/lab_host="XL10-Gold"
/notes="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream of EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

BASE COUNT
ORIGIN
69 a 138 c 180 g 68 t

Query Match 66.1% Score 15.2: DB 14: Length 455:
Best Local Similarity 47.8%: Pred No. 2.3e+03:
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRA5MANCCRSYTC 23
Db 287 CAGACGGCGAGACCCGCCCTC 265

RESULT 15
LOCUS A2560473/c 457 bp DNA linear GSS 20-NOV-2000
DEFINITION RPCI-23-180N17.TJ RPCI-23 Mus musculus genomic clone RPCI-23-180N17
, DNA sequence.
A2560473
A2560473 GI:11240293
GSS.
SOURCE
ORGANISM
Mus musculus.
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 457)
Zhao, S., Nieman, W., Feldblum, T., Malek, J., Shatsman, S., Akinet,
B., Levins, M., McGann, S., Tesgaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSS: RPCI-23-180N17.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@edlong.med.buitalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buitalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 180 row: N column: 17
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..457
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-180N17"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

```

BASE COUNT 149 a 89 c 85 g 134 t
ORIGIN

Query Match 66.1%; Score 15.2; DB 17; Length 457;
Best Local Similarity 47.8%; Pred. No. 2.3e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANNCKRAASMANCCNRSYTC 23
|||::||::||::||
Db 157 CACATCTAATACCCACCCAGCTC 135

Search completed: March 10, 2003, 06:42:46
Job time : 1341 secs

GenCore version 5.1.4_p5-4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:19:34 ; Search time 39.5 Seconds

(without alignments)
178,571 Million cell updates/sec

Title: US-09-975-842-2

Sequence: 1 gcn2_6/prodata/1/lna/5A.COMB.seq:*

Scoring table: IDENTITY_NUC

Gap: 10.0, Gapext 1.0

Searched: 441363 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents_NA:*

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21: /gcn2_6/prodata/1/lna/5A.COMB.seq:*

22: /gcn2_6/prodata/1/lna/5B.COMB.seq:*

23: /gcn2_6/prodata/1/lna/5A.COMB.seq:*

24: /gcn2_6/prodata/1/lna/5B.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	15.4	67.0	23	1	US-08-724-194-9
2	15.4	67.0	23	4	US-09-171-482-5
3	15.4	67.0	961	4	US-08-846-826A-3
4	15.4	67.0	968	4	US-08-846-826A-1
5	15.4	67.0	994	2	US-08-860-577-7
6	15.4	67.0	1080	3	US-09-043-627-1
7	15.4	67.0	1096	3	US-09-043-627-7
8	15.4	67.0	1098	3	US-09-043-627-5
9	15.4	67.0	1104	3	US-09-043-627-3
10	15.4	67.0	1113	2	US-08-860-577-9
11	15.4	67.0	1184	2	US-08-860-577-1
12	15.4	67.0	1203	2	US-08-860-577-1
13	15.4	67.0	1800	1	US-07-809-457A-8
14	15.4	67.0	1800	1	US-08-553-943-8
15	15.4	67.0	1800	1	PCT-US91-09437-8
16	15.4	67.0	1878	1	US-08-724-194-3
17	15.4	67.0	1888	1	US-08-885-107-1
18	15.4	67.0	2040	2	US-08-695-412B-11
19	15.4	67.0	2040	4	US-09-255-154D-11
20	15.4	67.0	2230	4	US-08-578-313-24
21	15.4	67.0	4459	4	US-09-363-243-2
22	15.4	67.0	5613	2	US-08-463-418-1
23	15.4	67.0	7244	4	US-08-378-313-26
24	15.4	67.0	7587	4	US-08-378-313-22
25	15.4	67.0	9060	4	US-08-378-313-20
26	15.4	67.0	15397	2	US-08-673-768-1
27	15.4	67.0	15397	2	US-08-673-768-1

28	14.4	62.6	70	4	US-09-364-380-27	Sequence 27, Appl
29	14.4	62.6	1155	2	US-08-331-644-4	Sequence 4, Appl
30	14.4	62.6	1155	5	PCT-US93-04102-4	Sequence 4, Appl
31	14.2	61.7	90	4	US-08-464-700-40	Sequence 40, Appl
32	14.2	61.7	92	4	US-08-464-700-15	Sequence 15, Appl
33	14.2	61.7	1497	2	US-08-632-598-1	Sequence 1, Appl
34	14.2	61.7	1712	2	US-09-231-240-1	Sequence 1, Appl
35	14.2	61.7	1712	4	US-08-724-194-1	Sequence 1, Appl
36	14.2	61.7	1945	1	US-08-464-700-53	Sequence 1, Appl
37	14.2	61.7	2210	4	US-08-641-627A-37	Sequence 37, Appl
38	14.2	61.7	2210	1	US-08-641-627A-39	Sequence 39, Appl
39	14.2	61.7	2427	2	US-08-724-194-7	Sequence 2, Appl
40	14.2	61.7	2678	2	US-08-724-194A-20	Sequence 20, Appl
41	14.2	61.7	246240	2	US-08-724-194A-21	Sequence 21, Appl
42	14.2	61.7	246240	2	US-08-724-194A-22	Sequence 22, Appl
43	14.2	61.7	246240	2	US-07-903-466-32	Sequence 32, Appl
44	14.2	61.7	246240	2	US-07-903-466-32	Sequence 32, Appl
45	13.8	60.0	238	1	US-07-903-466-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-724-194-9
Sequence 9, Application US/08724194
Patent No. 5824875
GENERAL INFORMATION:
APPLICANT: RANDU, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc-feature
LOCATION: group(3, 6, 9, 12, 18, 21)
OTHER INFORMATION: /note="N represents inosine"
US-08-724-194-9
Query Match 67.0%; Score 15.4; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGNATCCGNGTGTGNGTNG 23
DB 1 GGNATCCGNGTGTGNGTNG 23

RESULT 2
US-09-171-482-5
Sequence 5, Application US/09171482A
Patent No. 6184449
GENERAL INFORMATION:
APPLICANT: Ranu, Rajinder S.
TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
TITLE OF INVENTION: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES
FILE REFERENCE: TAGAMA-ROSE
CURRENT APPLICATION NUMBER: US/09/171,482A
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under WO98/14465; US5,824,875
EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Word Perfect 6.1
SEQ ID NO 5
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: 1
LOCATION: 3, 6, 9, 12, 18, and 21
OTHER INFORMATION: PCR primer
US-09-171-482-5

Query Match 67.0%; Score 15.4; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGNATCCGNGNTTNGNRTNG 23
DB 1 GGNATCCGNGNTTNGNRTNG 23

RESULT 3
US-08-846-826A-3
Sequence 3, Application US/08846826A
Patent No. 6194639
GENERAL INFORMATION:
APPLICANT: Botella, Jose
APPLICANT: Sanewski, Garth
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: One Commerce Square, 2005 Market Street, 22nd
STREET: Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,826A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9582
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S.
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
TELEFAX: 215-567-2991
TELEX: 831-494

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 961 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..102
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 103..194
FEATURE:
NAME/KEY: CDS
LOCATION: 195..961
US-08-846-826A-3

Query Match 67.0%; Score 15.4; DB 4; Length 961;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGNGNTTNGNRTNG 23
DB 567 GGGCTACGAGCTTTCGCGTCGG 589

RESULT 4
US-08-846-826A-1
Sequence 1, Application US/08846826A
Patent No. 6194639
GENERAL INFORMATION:
APPLICANT: Botella, Jose
APPLICANT: Sanewski, Garth
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: One Commerce Square, 2005 Market Street, 22nd
STREET: Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,826A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9582
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S.
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 968 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 1 968

Query Match 67.0%; Score 15.4; DB 4; Length 968;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCTTTCGAGTTGG 23
DB 571 GGCTTCCCGCTTTCGAGTTGG 593

RESULT 5

US-08-860-577-7
Sequence 7, Application US/03860577

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L.
APPLICANT: Deng, Rosaline Z.
APPLICANT: Carney, Kim J.
APPLICANT: Ruttenbiller, Glen E.

APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plants Expressing ACC

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESS: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite

STREET: 4700
CITY: Chicago

STATE: IL
COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:
- MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

* APPLICATION NUMBER: US/08/860,577
FILING DATE:

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V.
REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 994 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 3..975

US-08-860-577-7

Query Match 67.0%; Score 15.4; DB 2; Length 994;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCTTTCGAGTTGG 23
DB 621 GGCTTCCCGCTTTCGAGTTGG 643

RESULT 6

US-09-043-627-1
Sequence 1, Application US/09043627

Patent No. 6124525
GENERAL INFORMATION:

APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESS: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thaneet Circle, Suite 306

CITY: Princeton
STATE: NJ

COUNTRY: USA
ZIP: 08540-3662

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998

CLASSIFICATION: 800
PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996

PRIOR APPLICATION DATA: AU PN5559
FILING DATE: 20-SEP-1995

PRIOR APPLICATION DATA: AU PN5603
FILING DATE: 02-MAY-1996

ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.

REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555

TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1080 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS

LOCATION: 1..1080
US-09-043-627-1

Query Match 67.0%; Score 15.4; DB 3; Length 1080;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCTTTCGAGTTGG 23
DB 691 GGCTTCCCGCTTTCGAGTTGG 713

RESULT 7

US-09-043-627-7
Sequence 7, Application US/09043627

GENERAL INFORMATION:

APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESS: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thaneet Circle, Suite 306

CITY: Princeton
STATE: NJ

COUNTRY: USA
ZIP: 08540-3662

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043.627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
US-09-043-627-7

Query Match          67.0%; Score 15.4; DB 3; Length 1096;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGGNTYMGNTNG 23
DB 688 GGCCTCCCGCTTACGGGTGG 710

RESULT 8
US-09-043-627-5
Sequence 3, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanet Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043.627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1098
US-09-043-627-5

Query Match          67.0%; Score 15.4; DB 3; Length 1098;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATNCNGGNTYMGNTNG 23
DB 688 GGCCTCCCGGTTCCGGGTAGG 710

RESULT 9
US-09-043-627-3
Sequence 3, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanet Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043.627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
```

TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1104
US-09-043-627-3

Query Match 67.0%; Score 15.4; DB 3; Length 1104;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGATTAGAGTTGG 719
DB 697 GGATTCCTCGATTAGAGTTGG 719

RESULT 10
US-09-043-627-9
Sequence 9, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thane Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 23-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P95559
FILING DATE: 23-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P99603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1113
US-09-043-627-9

Query Match 67.0%; Score 15.4; DB 3; Length 1113;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGATTAGAGTTGG 719
DB 694 GGATTCCTCGATTAGAGTTGG 716

RESULT 11
US-08-860-577-1
Sequence 1, Application US/08860577
Patent No. 5998702
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
APPLICANT: Deng, Rosaline Z.
APPLICANT: Carney, Kim J.
APPLICANT: Rutencutter, Glen E.
APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plants Expressing ACC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamov & Katz, Ltd
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
STREET: 4700
CITY: Chicago
STATE: IL
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,577
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..39
FEATURE:
NAME/KEY: CDS
LOCATION: 135..433
FEATURE:
NAME/KEY: CDS
LOCATION: 595..1383
US-08-860-577-1

Query Match 67.0%; Score 15.4; DB 2; Length 1384;
Best Local Similarity 56.5%; Pred. No. 19;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGATTAGAGTTGG 23
DB 970 GGATTCCTCGATTAGAGTTGG 992

RESULT 12
US-08-378-313-18
Sequence 18, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO.: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1489
US-08-378-313-18

Query Match 67.0%; Score 15.4; DB 4; Length 1703;
Best Local Similarity 56.5%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNVTCNCNGNTTYMGNTNGC 23
DB 854 GGCCTCCGCTGCTTCGAGTGG 876

RESULT 13
US-07-809-457A-8
Sequence 8, Application US/07809457A
Patent No. 5512466
GENERAL INFORMATION:
APPLICANT: Kiese, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Monsanto Co. B94F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri

COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/809,457A
FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10538)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-07-809-457A-8

Query Match 67.0%; Score 15.4; DB 1; Length 1800;
Best Local Similarity 56.5%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNVTCNCNGNTTYMGNTNGC 23
DB 994 GGGTTCACAGATTTAGAGTCGG 1016

RESULT 14
US-08-553-943-8
Sequence 8, Application US/08553943
Patent No. 5702933
GENERAL INFORMATION:
APPLICANT: Kiese, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Monsanto Co. B94F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,943
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/809,457
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914

GenCore version 5.1.4-p5-4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:19:34 ; Search time 39.5 Seconds

(without alignments)
178,571 Million cell updates/sec

Title: US-09-975-842-3

Sequence: 1 cananncrasmancnrsytc 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issae3-Patents-NA:*

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5: /cgn2_6/ptcdat1/1na/PCrUS.COMB.seq:*
6: /cgn2_6/ptcdat1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	15.2	66.1	23	1	US-08-724-194-10 Sequence 10, Appl
2	15.2	66.1	23	4	US-09-171-482-6 Sequence 6, Appl
3	15.2	66.1	1096	3	US-09-043-627-7 Sequence 7, Appl
4	15.2	66.1	1098	3	US-09-043-627-5 Sequence 5, Appl
5	15.2	66.1	1104	3	US-08-378-313-18 Sequence 18, Appl
6	15.2	66.1	1703	4	US-08-632-598-1 Sequence 1, Appl
7	15.2	66.1	1712	2	US-09-231-240-1 Sequence 1, Appl
8	15.2	66.1	1743	4	US-09-171-482-1 Sequence 8, Appl
9	15.2	66.1	1800	1	US-07-809-457A8 Sequence 8, Appl
10	15.2	66.1	1800	1	US-08-553-943A8 Sequence 8, Appl
11	15.2	66.1	1800	5	PCT-US91-09437-8 Sequence 8, Appl
12	15.2	66.1	1800	5	US-08-724-194-3 Sequence 1, Appl
13	15.2	66.1	1878	1	US-08-483-107-1 Sequence 1, Appl
14	15.2	66.1	1888	1	US-08-724-194-11 Sequence 11, Appl
15	15.2	66.1	1945	2	US-08-695-412B-11 Sequence 11, Appl
16	15.2	66.1	2040	2	US-08-253-154D-11 Sequence 24, Appl
17	15.2	66.1	2230	4	US-08-378-313-24 Sequence 2, Appl
18	15.2	66.1	2613	1	US-08-724-194-2 Sequence 1, Appl
19	15.2	66.1	2613	1	US-08-463-418-1 Sequence 26, Appl
20	15.2	66.1	7244	4	US-08-378-313-26 Sequence 22, Appl
21	15.2	66.1	7587	4	US-08-378-313-22 Sequence 20, Appl
22	15.2	66.1	9060	2	US-08-673-768-1 Sequence 1, Appl
23	15.2	66.1	15397	2	US-08-673-768-1 Sequence 1, Appl
24	15.2	66.1	15397	2	US-08-860-577-11 Sequence 11, Appl
25	15.2	66.1	1497	2	US-08-860-577-11 Sequence 577, App
26	14.2	61.7	1497	2	US-08-860-577-11 Sequence 577, App
27	14	60.9	4712	4	US-09-221-017B-577 Sequence 577, App

C 28	14	60.9	11613	1	US-08-484-044-10 Sequence 10, Appl
C 29	13.6	59.1	720	3	US-09-306-881-3 Sequence 3, Appl
C 30	13.6	59.1	1200	4	US-09-327-681-5 Sequence 5, Appl
C 31	13.6	59.1	2832	4	US-09-397-885-6 Sequence 6, Appl
C 32	13.6	59.1	3033	1	US-08-453-695A-111 Sequence 111, App
C 33	13.6	59.1	3033	1	US-08-268-161A-111 Sequence 111, App
C 34	13.6	59.1	3033	2	US-08-453-702A-111 Sequence 111, App
C 35	13.6	59.1	3033	4	US-09-099-639-111 Sequence 111, App
C 36	13.6	59.1	3033	5	PCT-US95-08071-111 Sequence 111, App
C 37	13.6	59.1	4459	4	US-09-363-243-2 Sequence 49, Appl
C 38	13.6	59.1	4791	4	US-08-949-155-49 Sequence 49, Appl
C 39	13.6	59.1	4791	4	US-09-819-964-49 Sequence 19, Appl
C 40	13.6	59.1	10504	4	US-09-423-744A-19 Sequence 1, Appl
C 41	13.6	59.1	12143	4	US-09-423-744A-19 Sequence 15, Appl
C 42	13.2	57.4	20	3	US-09-043-627-15 Sequence 3, Appl
C 43	13.2	57.4	961	4	US-08-846-826A-3 Sequence 1, Appl
C 44	13.2	57.4	961	4	US-08-846-826A-3 Sequence 1, Appl
C 45	13.2	57.4	998	1	US-08-553-516-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-724-194-10
Sequence 10, Application US/08724194
Patent No. 5824875
GENERAL INFORMATION:
APPLICANT: RAND, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOACIDOPROBANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESS: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc-feature
LOCATION: group(3, 5, 6, 15, 18)
OTHER INFORMATION: /note="N represents Inosine"
US-08-724-194-10
Query Match 66.1%; Score 15.2; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CANANCKRAASMANCCNRSYTC 23
Db 1 CANANCKRAASMANCCNRSYTC 23

RESULT 2
US-09-171-482-6
Sequence 6, Application US/09171482A
Patent No. 6184449
GENERAL INFORMATION:
APPLICANT: Ranu, Rajinder S.
TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
TITLE OF INVENTION: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES
FILE REFERENCE: TAGAWA-ROSE
CURRENT APPLICATION NUMBER: US/09/171,482A
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under WO98/14465; US5,824,875
EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Word Perfect 6.1
SEQ ID NO 6
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: 1
LOCATION: 3, 5, 6, 15, and 18
OTHER INFORMATION: PCR primer
US-09-171-482-6

Query Match 66.1%; Score 15.2; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CANANCKRASMNCNRSYTC 23
Db 1 CANANCKRASMNCNRSYTC 23

RESULT 3
US-09-043-627-7/C
Sequence 7, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thonet Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELEPHONE/DOCKET NUMBER: 3573-11US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
US-09-043-627-7

Query Match 66.1%; Score 15.2; DB 3; Length 1096;
Best Local Similarity 47.8%; Pred. No. 40;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMNCNRSYTC 23
Db 1088 CAGACTGTGACCAACACGAGCTC 1066

RESULT 4
US-09-043-627-5/C
Sequence 5, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thonet Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

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LOCATION: 1.1098
US-09-043-627-5
Query Match
Best Local Similarity 66.1%; Score 15.2; DB 3; Length 1098;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMANCNRSYTC 23
Db 1091 CAACTCTGACGACCCGCGCTC 1069

RESULT 5
US-09-043-627-3/c
Sequence 3, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanel Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-MAR-1998
APPLICATION NUMBER: US/09/043,627
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CD3
LOCATION: 1.1104
US-09-043-627-3

Query Match
Best Local Similarity 66.1%; Score 15.2; DB 3; Length 1104;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMANCNRSYTC 23
Db 1097 CAGACCGTGAACGACGAGTTC 1075

LOCATION: 1.1098
US-09-043-627-5
Query Match
Best Local Similarity 66.1%; Score 15.2; DB 3; Length 1098;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMANCNRSYTC 23
Db 1091 CAACTCTGACGACCCGCGCTC 1069

RESULT 6
US-08-378-313-18/c
Sequence 18, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 11.1489
US-08-378-313-18

Query Match
Best Local Similarity 66.1%; Score 15.2; DB 4; Length 1703;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASMANCNRSYTC 23
Db 1254 CAAACTCGAAACCAACCTGCGCTC 1232

RESULT 7
US-08-632-598-1/c
Sequence 1, Application US/08632598
Patent No. 5886164
GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHAN D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY AND CUSHMAN
STREET: 100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,598
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
TELEFAX: 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: MUSA
IMMEDIATE SOURCE:
CLONE: ACS GENE
US-08-632-598-1

Query Match 66.1% Score 15.2: DB 2: Length 1712;
Best Local Similarity 47.8% Pred. No. 43;
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CANANCKRASMNCNRSYTC 23
||| 1::||:| 11:::|1
Db 1265 CACACCTGACACCCCGGCTC 1243

RESULT 8
US-09-231-240-1/c
Sequence 1, Application US/09231240
Patent No. 6262346
GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY AND CUSHMAN
STREET: 1100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,240
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
```

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TELEFAX: 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: MUSA
IMMEDIATE SOURCE:
CLONE: ACS GENE
US-09-231-240-1

Query Match 66.1% Score 15.2: DB 4: Length 1712;
Best Local Similarity 47.8% Pred. No. 43;
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CANANCKRASMNCNRSYTC 23
||| 1::||:| 11:::|1
Db 1265 CACACCTGACACCCCGGCTC 1243

RESULT 9
US-09-171-482-1/c
Sequence 1, Application US/09171482A
Patent No. 6184449
GENERAL INFORMATION:
APPLICANT: RANU, Rajinder S.
TITLE OF INVENTION: A 1-MINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
FILE REFERENCE: JAGAMA-ROSE
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under WO98/14465; US5,824,87
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Word Perfect 6.1
SEQ ID NO 1
LENGTH: 1743
TYPE: DNA
ORGANISM: Rosa kardinal
US-09-171-482-1

Query Match 66.1% Score 15.2: DB 4: Length 1743;
Best Local Similarity 47.8% Pred. No. 43;
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CANANCKRASMNCNRSYTC 23
||| 1::||:| 11:::|1
Db 1628 CAAACCGGACCAATCCCGTTC 1606

RESULT 10
US-07-809-457A-8/c
Sequence 8, Application US/07809457A
Patent No. 5512466
GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. B84F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/809,457A
FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-07-809-457A-8

Query Match
Best Local Similarity 47.8%; DB 1; Length 1800;
Pred. No. 43;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRAASMANCNRSTYC 23
Db 1394 CAAACTCGAGACACCTGGCTC 1372

RESULT 11
US-08-553-943-8/c
Sequence 8, Application US/08553943
Patent No. 570293
GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,943
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/809,457
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-553-943-8

Query Match
Best Local Similarity 47.8%; DB 1; Length 1800;
Pred. No. 43;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRAASMANCNRSTYC 23
Db 1394 CAAACTCGAGACACCTGGCTC 1372

RESULT 12
PCT-US91-09437-8/c
Sequence 8, Application PC/TUS9109437
Patent No. 570293
GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09437
FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
PCT-US91-09437-8

Query Match
Best Local Similarity 47.8%; DB 5; Length 1800;
Pred. No. 43;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRAASMANCNRSTYC 23
Db 1394 CAAACTCGAGACACCTGGCTC 1372

RESULT 13
US-08-724-194-3/c
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Sequence 3, Application US/08724194
Patent No. 5824875
GENERAL INFORMATION:
APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARONITUM TO CONTROL ETHYLENE LEVELS
TITLE OF INVENTION: IN GERANIUMS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1878 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-724-194-3

Query Match 66.1%; Score 15.2; DB 1; Length 1878;
Best Local Similarity 47.8%; Pred. No. 44;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANNCKRAASMANCNSRYTC 23
US-08-485-107-1/c
Db 1353 CACACTCTAACCCCTGCTC 1331

RESULT 14
US-08-485-107-1/c
Sequence 1, Application US/08485107
Patent No. 5767376
GENERAL INFORMATION:
APPLICANT: STILES, JOHN I.
APPLICANT: NEUPANE, KABI R.
TITLE OF INVENTION: ACC SYNTHASE GENE AND ITS USE IN PLANTS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAYERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,107
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 08-01170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1888 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 17..1480
US-08-485-107-1

Query Match 66.1%; Score 15.2; DB 1; Length 1888;
Best Local Similarity 47.8%; Pred. No. 44;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANNCKRAASMANCNSRYTC 23
Db 1254 CAACCCCTGAACCCAGCAGTTC 1232

RESULT 15
US-08-724-194-1/c
Sequence 1, Application US/08724194
Patent No. 5824875
GENERAL INFORMATION:
APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARONITUM TO CONTROL ETHYLENE LEVELS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-724-194-1

Query Match 66.1%; Score 15.2; DB 1; Length 1945;
Best Local Similarity 47.8%; Pred. No. 44;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANNCKRAASMANCNSRYTC 23
Db 1353 CACACTCTAACCCCTGCTC 1331

Mon Mar 10 03:10:49 2003

us-09-975-842-3.mli

Page 7

Db 1315 CAAACCTAAGCAACCCGGCTC 1293

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Job time : 44 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:25:27 ; Search time 50.5 Seconds
(without alignments)
304.201 Million cell updates/sec

Title: US-C9-975-842-2

Sequence: 1 ggnntcncngnttymcrrtng 23

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 478924 seqs, 33395956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_NA:

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3: /cgn2_6/ptodata1/pubna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata1/pubna/US06_PUBCOMB.seq:*
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13: /cgn2_6/ptodata1/pubna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	15.4	67.0	23	US-09-776-529A-5	Sequence 5, Appl1
2	15.4	67.0	748	US-09-770-149-16	Sequence 16, Appl1
3	15.4	67.0	1344	US-09-938-842A-1571	Sequence 1571, Ap
4	14.4	62.6	274	US-09-294-093B-4729	Sequence 4729, Ap
5	14.4	62.6	1506	US-09-963-285-9	Sequence 9, Appl1
6	14.4	62.6	2712	US-09-963-285-6	Sequence 6, Appl1
7	14.4	62.6	3289	US-09-963-285-8	Sequence 8, Appl1
8	14.4	62.6	4158	US-09-963-285-3	Sequence 3, Appl1
9	14.4	62.6	6021	US-09-963-285-5	Sequence 5, Appl1
10	14.4	62.6	6458	US-09-963-285-1	Sequence 1, Appl1
11	14.2	61.7	536	US-09-974-879-57	Sequence 57, Appl1
12	14.2	61.7	1488	US-09-938-842A-1726	Sequence 1726, Ap
13	14.2	61.7	2099	US-09-822-830A-14	Sequence 14, Appl1
14	14.2	61.7	2242	US-09-954-456-542	Sequence 542, Appl1
15	14.2	61.7	2274	US-09-921-771-5	Sequence 5, Appl1
16	14.2	61.7	14962	US-09-764-878-244	Sequence 244, Appl1
17	14.2	61.7	15849	US-09-880-107-362	Sequence 2362, Ap
18	13.8	60.0	363	US-09-864-761-24268	Sequence 24268, Ap
19	13.8	60.0	421	US-09-925-299-409	Sequence 409, Appl1

C	20	13.8	60.0	421	10	US-09-925-299-409	Sequence 409, Appl1
C	21	13.8	60.0	574	10	US-09-864-761-13696	Sequence 13696, A
C	22	13.8	60.0	594	10	US-09-864-761-7563	Sequence 7563, Ap
C	23	13.8	60.0	3015	9	US-10-161-510-6	Sequence 6, Appl1
C	24	13.8	60.0	22161	10	US-09-764-847-1020	Sequence 1020, Ap
C	25	13.8	60.0	110096	10	US-09-880-107-1542	Sequence 1542, Ap
C	26	13.4	58.3	308	10	US-09-867-701-3531	Sequence 3531, Ap
C	27	13.4	58.3	451	10	US-09-876-889-320	Sequence 923, Appl1
C	28	13.4	58.3	609	10	US-09-833-381-293	Sequence 293, Appl1
C	29	13.4	58.3	833	10	US-09-974-300-293	Sequence 1, Appl1
C	30	13.4	58.3	1743	10	US-09-776-529A-3	Sequence 3442, Ap
C	31	13.4	58.3	1985	10	US-09-880-107-3442	Sequence 1, Appl1
C	32	13.4	58.3	2093	12	US-10-044-090-292	Sequence 292, Ap
C	33	13.4	58.3	4485	9	US-10-002-974-1	Sequence 1, Appl1
C	34	13.4	58.3	4485	12	US-10-014-265-33	Sequence 33, Appl1
C	35	13.4	58.3	4486	9	US-10-014-265-33	Sequence 261, Appl1
C	36	13.4	58.3	4486	12	US-09-764-878-261	Sequence 261, Appl1
C	37	13.4	58.3	23626	10	US-09-764-860-940	Sequence 240, Appl1
C	38	13.4	58.3	23632	10	US-09-764-878-262	Sequence 941, Appl1
C	39	13.4	58.3	23632	10	US-09-764-860-941	Sequence 3, Appl1
C	40	13.4	58.3	172637	10	US-09-805-458A-3	Sequence 10488, A
C	41	13.4	57.4	375	10	US-09-783-590-10488	Sequence 18, Appl1
C	42	13.2	57.4	1122	9	US-10-060-432-18	Sequence 18, Appl1
C	43	13.2	57.4	1122	10	US-09-905-173-18	Sequence 186, Appl1
C	44	13.2	57.4	1122	10	US-09-738-626-186	
C	45	13.2	57.4	1374	9	US-09-738-626-186	

ALIGNMENTS

RESULT 1
US-09-776-529A-5
Sequence 5, Application US/09776529A
Patent No. US20020083484A1
GENERAL INFORMATION:
APPLICANT: Tagawa Greenhouses, Inc.
TITLE OF INVENTION: A 1-Aminoacylpropane-1-Carboxylate Synthase Gene From Rosa to
FILE REFERENCE: Tagawa-Rose
CURRENT APPLICATION NUMBER: US/09/776,529A
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 08/724,194
PRIOR FILING DATE: 1996-10-01
PRIOR APPLICATION NUMBER: US 09/171,482
PRIOR FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: PCT/US97/17644
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc-feature
LOCATION: (3), (6), (9), (12), (18), and (21)
OTHER INFORMATION: n=1
US-09-776-529A-5
Query Match 67.0%; Score 15.4; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ox 1 GGNNTCNCNGNTTymcrrtng 23
Db 1 GGNNTCNCNGNTTymcrrtng 23
RESULT 2
US-09-770-149-16/c

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; Sequence 16, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matchew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(748)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-16

Query Match          67.0%; Score 15.4; DB 10; Length 748;
Best Local Similarity 56.5%; Pred. No. 40;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 GGNYNCCGNGNTTYMGNRTNG 23
Db      617 GGTCTTCTGCTTCCGCGTGG 595

RESULT 3
US-09-938-842A-1571
; Sequence 1571, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1571
; LENGTH: 1344
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1571

Query Match          67.0%; Score 15.4; DB 9; Length 1344;
Best Local Similarity 56.5%; Pred. No. 44;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 GGNYNCCGNGNTTYMGNRTNG 23
Db      862 GGTCTTCTGCTTCCGCGTGG 884

RESULT 4
US-09-294-093B-4729/C
; Sequence 4729, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4729
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incycle ID No. US20010051335A1 700354878H1
; LOCATION: 146, 203, 223
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4729

Query Match          62.6%; Score 14.4; DB 10; Length 274;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 GNYTNCNGNGNTTYMGNRTNG 23
Db      60 GTTCCAGGCTTCAGCATGG 39

RESULT 5
US-09-963-285-9
; Sequence 9, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbäck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1506
```

```

: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1503)
US-09-963-285-9

```

```

Query Match      62.6%; Score 14.4; DB 10; Length 1506;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      1 GGNNTCCNGGNTTYMGNTNG 22
      ||:|||||:|:|:|:|:|
Db      796 GGGCTGCCCTGGCTTCAGCGTGG 817

```

```

RESULT 6
US-09-963-285-6
: Sequence 6, Application US/09963285
: Patent No. US20020090707A1
: GENERAL INFORMATION:
: APPLICANT: Enerbck, Sven
: APPLICANT: Kirook, Katarina
: APPLICANT: Rondahl, Lena
: APPLICANT: Wasserman, Wyeth
: TITLE OF INVENTION: PROMOTER SEQUENCES
: FILE REFERENCE: 13425-042001
: CURRENT APPLICATION NUMBER: US/09/963,285
: PRIORITY FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: SE 0004102-0
: PRIOR FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: US 60/238,897
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: SE 0003435-5
: PRIOR FILING DATE: 2000-09-26
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 2712
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (422)...(1903)
US-09-963-285-6

```

```

Query Match      62.6%; Score 14.4; DB 10; Length 2712;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      1 GGNNTCCNGGNTTYMGNTNG 22
      ||:|||||:|:|:|:|:|
Db      1214 GGGCTGCCCTGGCTTCAGCGTGG 1235

```

```

RESULT 7
US-09-963-285-8
: Sequence 8, Application US/09963285
: Patent No. US20020090707A1
: GENERAL INFORMATION:
: APPLICANT: Enerbck, Sven
: APPLICANT: Kirook, Katarina
: APPLICANT: Rondahl, Lena
: APPLICANT: Wasserman, Wyeth
: TITLE OF INVENTION: PROMOTER SEQUENCES
: FILE REFERENCE: 13425-042001
: CURRENT APPLICATION NUMBER: US/09/963,285
: PRIORITY FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: SE 0004102-0
: PRIOR FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: US 60/238,897
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: SE 0003435-5

```

```

: PRIOR FILING DATE: 2000-09-26
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 3289
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-963-285-8

```

```

Query Match      62.6%; Score 14.4; DB 10; Length 3289;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      1 GGNNTCCNGGNTTYMGNTNG 22
      ||:|||||:|:|:|:|:|
Db      1992 GGGCTGCCCTGGCTTCAGCGTGG 2013

```

```

RESULT 8
US-09-963-285-3
: Sequence 3, Application US/09963285
: Patent No. US20020090707A1
: GENERAL INFORMATION:
: APPLICANT: Enerbck, Sven
: APPLICANT: Kirook, Katarina
: APPLICANT: Rondahl, Lena
: APPLICANT: Wasserman, Wyeth
: TITLE OF INVENTION: PROMOTER SEQUENCES
: FILE REFERENCE: 13425-042001
: CURRENT APPLICATION NUMBER: US/09/963,285
: PRIORITY FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: SE 0004102-0
: PRIOR FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: US 60/238,897
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: SE 0003435-5
: PRIOR FILING DATE: 2000-09-26
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 4158
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (187)...(1437)
US-09-963-285-3

```

```

Query Match      62.6%; Score 14.4; DB 10; Length 4158;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      1 GGNNTCCNGGNTTYMGNTNG 22
      ||:|||||:|:~|:|:|:|
Db      730 GGGCTGCCCTGGCTTCAGCGTGG 751

```

```

RESULT 9
US-09-963-285-5
: Sequence 5, Application US/09963285
: Patent No. US20020090707A1
: GENERAL INFORMATION:
: APPLICANT: Enerbck, Sven
: APPLICANT: Kirook, Katarina
: APPLICANT: Rondahl, Lena
: APPLICANT: Wasserman, Wyeth
: TITLE OF INVENTION: PROMOTER SEQUENCES
: FILE REFERENCE: 13425-042001
: CURRENT APPLICATION NUMBER: US/09/963,285
: PRIORITY FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: SE 0004102-0
: PRIOR FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: US 60/238,897

```

```
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6021
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1649)...(438)
US-09-963-285-5

Query Match          62.6%; Score 14.4; DB 10; Length 6021;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCGTTCAGCGTGG 2883
Db 2862 GGGCTGCCCGGCTTCAGCGTGG 2883

RESULT 10
US-09-963-285-1
; Sequence 1, Application US/09963285
; Patent No. US2002090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbeck, Sven
; APPLICANT: Krook, Katrina
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963.285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2235)...(3737)
US-09-963-285-1

Query Match          62.6%; Score 14.4; DB 10; Length 6458;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCGTTCAGCGTGG 3051
Db 3030 GGGCTGCCCGGCTTCAGCGTGG 3051

RESULT 11
US-09-974-879-57
; Sequence 57, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020F2
; CURRENT APPLICATION NUMBER: US/09/974,879
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
```

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; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (536)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-974-879-57

Query Match          61.7%; Score 14.2; DB 9; Length 536;
Best Local Similarity 56.5%; Pred. No. 1.7e+02;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 GGNATCCGCGTTCAGCGTGG 23
Db 295 GGGTTKCCAGGCTTCAGGCGTGG 317

RESULT 12
US-09-938-842A-1726
; Sequence 1726, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
```

;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 1726
;; LENGTH: 1488
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1726

Query Match
Best Local Similarity 56.5%; Pred. No. 1.9e+02;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 847 GGCTGCCGCTGTAGAGTTGG 869

RESULT 13
US-09-822-830A-14

;; Sequence 14, Application US/09822830A
;; Patent No. US20020142952A1
;; GENERAL INFORMATION:
;; APPLICANT: Genetics Institute, Inc.
;; APPLICANT: Wong, Gordon G.
;; APPLICANT: Clark, Hilary
;; APPLICANT: Fechtel, Kim
;; APPLICANT: Agostino, Michael J.
;; APPLICANT: Howes, Steven H.
;; APPLICANT: Resnick, Richard J.
;; APPLICANT: Gulukota, Kamalakari
;; APPLICANT: Graham, James R.
;; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
;; FILE REFERENCE: G/N 6402
;; CURRENT APPLICATION NUMBER: US/09/822,830A
;; CURRENT FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195,604
;; PRIOR FILING DATE: 2000-04-06
;; NUMBER OF SEQ ID NOS: 631
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 2099
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-822-830A-14

Query Match
Best Local Similarity 61.7%; Score 14.2; DB 10; Length 2099;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 1639 GGCTTCCGAGCTTGAGAGTGG 1661

RESULT 14
US-09-954-456-542

;; Sequence 542, Application US/09954456
;; Patent No. US2002011507A1
;; GENERAL INFORMATION:
;; APPLICANT: Young, Paul
;; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
;; FILE REFERENCE: 689290-76
;; CURRENT APPLICATION NUMBER: US/09/954,456
;; CURRENT FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: US/60/233,617
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US/60/234,052
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: US/60/234,923
;; PRIOR FILING DATE: 2000-09-25

;; PRIOR APPLICATION NUMBER: US/60/235,134
;; PRIOR FILING DATE: 2000-09-25
;; PRIOR APPLICATION NUMBER: US/60/235,637
;; PRIOR FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US/60/235,638
;; PRIOR FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US/60/235,711
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,720
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,840
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,863
;; PRIOR FILING DATE: 2000-09-27
;; NUMBER OF SEQ ID NOS: 2276
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 542
;; LENGTH: 2242
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-954-456-542

Query Match
Best Local Similarity 56.5%; Pred. No. 2e+02; DB 10; Length 2242;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 1256 GGCTTCCGAGCTTGAGTGG 1278

RESULT 15
US-09-921-771-5

;; Sequence 5, Application US/09921771
;; Patent No. US20020081284A1
;; GENERAL INFORMATION:
;; APPLICANT: Li, Dean Y.
;; TITLE OF INVENTION: Manipulation of Arterial-Venous Identity
;; FILE REFERENCE: 10402-011
;; CURRENT APPLICATION NUMBER: US/09/921,771
;; CURRENT FILING DATE: 2001-08-03
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 2274
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-921-771-5

Query Match
Best Local Similarity 61.7%; Score 14.2; DB 10; Length 2274;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 1207 GGCTTCCGAGCTTGAGTGG 1229

Search completed: March 10, 2003, 06:46:24
Job time : 63.5 secs

